



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 179881

TO: Christian Fronda
Location: 2d78 / 2c70
Thursday, March 02, 2006
Art Unit: 1652
Phone: 571-272-0929
Serial Number: 10 / 014774

From: Jan Delaval
Location: Biotech-Chem Library
Remsen 1a51
Phone: 571-272-2504

jan.delaval@uspto.gov

Search Notes

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STIC-Biotech/ChemLib

179881

From: Fronda, Christian
Sent: Friday, February 17, 2006 9:56 AM
To: STIC-Biotech/ChemLib
Subject: RE: Score Over Length Sequence Searches for Serial NO. 10/014,774

Importance: High

Sorry for my mistake. The correct case is Serial No. 10/014,774.

I have made the corrections to the original email below. Thank you.

Christian L. Fronda
Art Unit 1652
Office REM 2D78
Mailbox REM 2C70
(571)272-0929

RECEIVED
FEB 17 2006
(STIC)

-----Original Message-----

From: STIC-Biotech/ChemLib
Sent: Friday, February 17, 2006 9:50 AM
To: Fronda, Christian
Subject: RE: Score Over Length Sequence Searches for Serial NO. 10/014,744

There is no valid CRF for this serial number, please provide us with another valid serial number. Thank you

-----Original Message-----

From: Fronda, Christian
Sent: Friday, February 17, 2006 9:39 AM
To: STIC-Biotech/ChemLib
Subject: Score Over Length Sequence Searches for Serial NO. 10/014,774
Importance: High

Score over Length Searches for Serial No. 10/014,774

1. Please do a score over length search on SEQ ID NO: 1, minimum length 10, maximum length 1036 , with a score/length value = 1 (i.e. % match = 100)

Please search against nucleic acid commercial, PGPub, issued, and interference databases.

SAVE 50 Hits, if available.

2. Please do a score over length search on SEQ ID NO: 3, minimum length 10, maximum length 970 , with a score/length value = 1 (i.e. % match = 100)

Please search against nucleic acid commercial, PGPub, issued, and interference databases.

SAVE 50 Hits, if available.

Searcher: [Signature]
Searcher Phone: 22504
Date Searcher Picked up: 2/28/06
Date completed: 3/2/06
Searcher Prep Time: 20
Online Time: 150

Type of Search
NA# 14 AA#
S/L: ✓ Oligomer: ✓
Encode/Transl:
Structure #: Text:
Inventor: Litigation:

Vendors and cost where applicable
STN:
DIALOG:
QUESTEL/ORBIS:
LEXIS/NEXIS:
SEQUENCE SYSTEM: ✓
WWW/Internet:
Other (Specify):

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 2, 2006, 10:50:59 ; Search time 1 Seconds
(without alignments)
3.181 Million cell updates/sec

Title: US-10-014-774-1

Perfect score: 1036

Sequence: 1 cccgtgacggcttgag.....gagaaaaaaaaaaaaa 1036

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 0.5

Searched: 2 seqs, 1535 residues

Total number of hits satisfying chosen parameters: 4

Minimum DB seq length: 10

Maximum DB seq length: 1036

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 2 summaries

Database : us-10-014-774-1.sl.rge4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1036	100.0	1036	1 AX045359	ACCESSION:AX045359
2	487.5	47.1	499	1 AX045372	ACCESSION:AX045372

ALIGNMENTS

RESULT 1
AX045359
LOCUS AX045359 1036 bp DNA linear PAT 24-NOV-2000
DEFINITION Sequence 1 from Patent WO0066733.
ACCESSION AX045359
VERSION AX045359.1 GI:11343859

KEYWORDS Mus sp.
SOURCE Mus sp.
ORGANISM Mus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE 1
D'Azzo, A., Bongiovanni, A. and Nastasi, T.
AUTHORS Protein specific for cardiac and skeletal muscle
TITLE Patent: WO 0066733-A 1 09-NOV-2000;
JOURNAL ST. JUDE CHILDREN'S RESEARCH HOSPITAL (US)

FEATURES
Location/Qualifiers
source
1..1036
/organism="Mus sp."
/mol_type="unassigned DNA"
/db_xref="taxon:10095"

Query Match 100.0%; Score 1036; DB 1; Length 1036;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1036; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB	1	CCCTGTTGCACGGCTTGGAGATGGCTCTCCCTCCGAAACACGTAGGACTGGGTGCCCCAC	60
QY	61	GGAGCCCTGGCGCCGAGAGCCCTCCGACCCGCTTCCACCAAGTGCATGGAGCCCAACA	120
DB	61	GGAGCCCTGGCGCCGAGAGCCCTCCGACCCGCTTCCACCAAGTGCATGGAGCCCAACA	120
QY	121	TCCGCATGGAGCCCTCAGGAAACGAGCCACACGCGTGGAGAGTTTCCGCCACCGTGTGT	180
DB	121	TCCGCATGGAGCCCTCAGGAAACGAGCCACACGCGTGGAGAGTTTCCGCCACCGTGTGT	180
QY	181	GCTTCAGTCTGTGAGCCCTCGCCCGCCGAGGATTTCTAGTGGAAATTCAGGAAAGA	240
DB	181	GCTTCAGTCTGTGAGCCCTCGCCCGCCGAGGATTTCTAGTGGAAATTCAGGAAAGA	240
QY	241	AGCTGGGCTGGTGGGGCACCCTAGCTCTGGCCCTGACGCTCTGGATCCCGCCAGTCTGG	300
DB	241	AGCTGGGCTGGTGGGGCACCCTAGCTCTGGCCCTGACGCTCTGGATCCCGCCAGTCTGG	300
QY	301	CCGCTGTACCCGAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	360
DB	301	CCGCTGTACCCGAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	360
QY	361	CTATCACACGCCACCAACACCGTGTGCGCCGCGGAGGTCAACAGAGCGGAGGAGCGG	420
DB	361	CTATCACACGCCACCAACACCGTGTGCGCCGCGGAGGTCAACAGAGCGGAGGAGCGG	420
QY	421	TCCCGAGTGTGCTCCCAAGCCCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	480
DB	421	TCCCGAGTGTGCTCCCAAGCCCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	480
QY	481	TTCCCGGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	540
DB	481	TTCCCGGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	540
QY	541	AGCTCTATGAACAAAAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	600
DB	541	AGCTCTATGAACAAAAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	600
QY	601	TCTGCCCGCTGAGGATGGGACCGCGGACATGACATCATCAACGCGGAGGAGCATGG	660
DB	601	TCTGCCCGCTGAGGATGGGACCGCGGACATGACATCATCAACGCGGAGGAGCATGG	660
QY	661	GCCCTAGCGCCGCGGGGCTGCGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	720
DB	661	GCCCTAGCGCCGCGGGGCTGCGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	720
QY	721	CTTCCACCAAGAGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	780
DB	721	CTTCCACCAAGAGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	780
QY	781	TGTGCCGACTAGTATCCAGAGAGGGTGTACACAGGCTGGCCATTGATGTGCTCCACC	840
DB	781	TGTGCCGACTAGTATCCAGAGAGGGTGTACACAGGCTGGCCATTGATGTGCTCCACC	840
QY	841	TGCCCAAAAGGACTGAAGACTTCTGCAAGTACGATGAACGATGAACGCTGTCTGTGG	900
DB	841	TGCCCAAAAGGACTGAAGACTTCTGCAAGTACGATGAACGATGAACGCTGTCTGTGG	900
QY	901	CCACGAGAGCAAGTCCCGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGG	960
DB	901	CCACGAGAGCAAGTCCCGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGG	960
QY	961	TGGTGGCAGCTCACAAATCAGGGCTGGAAATAAATAGAGCCGATGTGGATTTCTGAGA	1020
DB	961	TGGTGGCAGCTCACAAATCAGGGCTGGAAATAAATAGAGCCGATGTGGATTTCTGAGA	1020
QY	1021	AAAAAAAAAAAAAAAAAAAA 1036	
DB	1021	AAAAAAAAAAAAAAAAAAAA 1036	

```
RESULT 2
AX045372/c
LOCUS      AX045372      499 bp      DNA      linear      PAT 24-NOV-2000
DEFINITION Sequence 14 from Patent WO0066733.
ACCESSION  AX045372
VERSION     AX045372.1  GI:11343862
KEYWORDS
SOURCE      Mus sp.
ORGANISM    Mus sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1
AUTHORS    D'Azzo, A., Bongiovanni, A. and Nastasi, T.
TITLE      Protein specific for cardiac and skeletal muscle
JOURNAL    Patent: WO 0066733-A 14 09-NOV-2000;
            ST. JUDE CHILDREN'S RESEARCH HOSPITAL (US)
FEATURES   Location/Qualifiers
            source          1..499
                        /organism="Mus sp."
                        /mol_type="unassigned DNA"
                        /db_xref="taxon:10095"
Query Match      47.1%; Score 487.5; DB 1; Length 499;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 498; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
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DB      499  GTCTTGGCCTGACCGCTCTGGATCCCGCCAGTCTGGCGGCTGTACCCGAGTTTTCACCTGC 440
QY      325  CTGACTTGGTCAGCCTTGGCCACAGTTGGGTCTTCGCTATCACACGCCACCAACCGTG 384
DB      439  CTGACTTGGTCAGCCTTGGCCACAGTTGGGTCTTCGCTATCACACGCCACCAACCGTG 380
QY      385  TGCCCCGGGAGGTCACCCAGAGCGGAGCGGTCGCCAGTGGTCCCGAGCCCTAC 444
DB      379  TGCCCCGGGAGGTCACCCAGAGCGGAGCGGTCGCCAGTGGTCCCGAGCCCTAC 320
QY      445  TGGTTGAACCCCTATCTCGCATCGAGCAGTTCCGAATTCGCCGGACCGTCTGGTGGGCC 504
DB      319  TGGTTGAACCCCTATCTGGCATCGAGCAGTTCCGAATTCGCCGGACCGTCTGGTGGGCC 260
QY      505  GCAGCCGGCCAGGCTTTATAGCCACCTCTTTAGATCAGCTCTATGAACAAACCGTGTGC 564
DB      259  GCAGCCGGCCAGGCTTTATAGCCACCTCTTAGATCAGCTCTATGAACAAACCGTGTGC 200
QY      565  CTCCTACAGCGCGCGAGCGCTTGGGTGTTCTCTTCTGCCCGCTGAGGATGGGACCG 624
DB      199  CTCCTACAGCGCGCGAGCGCTTGGGTGTTCTCTTCTGCCCGCTGAGGATGGGACCG 140
QY      625  CCGACATGCATCATCATCAACGGGAGGACATGGGCCCTTAGCGCCCGGGGGCTGCCAG 684
DB      139  CCGACATGCATCATCATCAACGGGAGGACATGGGCCCTTAGCGCCCGGGGGCTGCCAG 80
QY      685  CTGCTCAGCCCTCTACGCTGTGTAGATGTGTTGTTCACCAAGAGCGT-GCGTCTG 743
DB      79   CTGCTCAGCCCTCTACGCTGTGTAGATGTGTTGTTCACCAAGAGCGTGGCGTCTG 20
QY      744  GTCCAGCTGGAGTATGGCT 762
DB      19  GTCCAGCTGGAGTATGGCT 1
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Search completed: March 2, 2006, 10:51:01
Job time : 2 secs

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 2, 2006, 10:53:08 ; Search time 4 Seconds
(without alignments)
3.741 Million cell updates/sec

Title: US-10-014-774-1
Perfect score: 1036
Sequence: 1 ccctgtgcagcgttgag.....gagagagagagagagagagag 1036

Scoring table: IDENTITY_NUC
Gapop 10.0 ; Gapext 0.5

Searched: 18 seqs, 7222 residues

Total number of hits satisfying chosen parameters: 36

Minimum DB seq length: 10
Maximum DB seq length: 1036

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 18 summaries

Database : us-10-014-774-1.sl.rst4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1006.6	97.2	1014	1	AK004524
C	660.6	63.8	684	1	CO039719
3	632.4	61.0	634	1	BE650303
C	442.2	42.7	457	1	BE956589
C	439.2	42.4	445	1	BY262946
C	430.2	41.5	443	1	AW124138
C	399.4	38.6	402	1	BY267664
8	366.8	35.4	384	1	BY105284
9	358.3	34.6	376	1	BY670130
C	334.4	32.3	336	1	AW125078
C	325.4	31.4	335	1	BE955244
C	320.8	31.0	326	1	BY781925
C	253.4	24.5	255	1	CL631771
14	249.8	24.1	257	1	CG487097
15	243.8	23.5	251	1	CG479214
C	224	21.6	228	1	EX632311
C	199	19.2	200	1	CX214893
18	188.6	18.2	195	1	AV022299

ALIGNMENTS

RESULT 1
AK004524
LOCUS: 1014 bp mRNA linear HTC 03-APR-2004
DEFINITION Mus musculus 18-day embryo whole body cDNA, RIKEN full-length enriched library, clone:1190009E12 product:hypothetical SOCS domain, C-terminus of STAT-inhibitors containing protein, full insert sequence.
ACCESSION AK004524
VERSION AK004524.1 GI:12835749
KEYWORDS HTC; CAP trapper.

SOURCE ORGANISM

Mus musculus (house mouse)
Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBLISHED

REFERENCE

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PUBLISHED

cleaved with XhoI and SstI. Cloning sites, 5' end: SstI; 3' end:
XhoI. Host: SOLR.

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polyA_site
1014
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Query Match 97.2%; Score 1006.6; DB 1; Length 1014;
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Matches 1009; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy 905 CAGAGCAAAAGTCCCGGCTGCTGCCTCTAGAGAAGTGGCTAGTCTGAAGCTGGT 964
Db 902 CAGAGCAAAAGTCCCGGCTGCTGCCTCTAGAGAAGTGGCTAGTCTGAAGCTGGT 961
Qy 965 CGCACAGCTCACAATCAGGCTGGAAATAAATAGACCGGATGGGATGTTCTG 1017
Db 962 CGCACAGCTCACAATCAGGCTGGAAATAAATAGACCGGATGGGATGTTCTG 1014

RESULT 2
CO039719/c
LOCUS
DEFINITION
684 bp mRNA linear EST 10-JUN-2004
UI-M-BH2.1-apr-e-06-0-UI.s1 NIH BMAP_M.S3.1 Mus musculus cDNA clone
UI-M-BH2.1-apr-e-06-0-UI 3', mRNA sequence.
CO039719
VERSION
KEYWORDS
EST.
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Murioidea; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 684)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
DNA sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/mousefl.html>
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
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FEATURES
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polylinker; Site 1: Not I; Site 2: Eco RI; The
NIH_BMAP_M.S3.1 library is a subtracted library of a

series, ultimately derived from a mixture of individually tagged normalized libraries from ten regions of the mouse brain (cerebellum, brain stems, olfactory bulbs, hypothalamus, cortex, amygdala, basal ganglia, pineal gland, striatum, hippocampus) after a series of subtractions to reduce the representation of cDNAs from which ESTs had already been generated. The following serially subtracted libraries were generated in this process: NIH_BMAP_M.S3.1, NIH_BMAP_M.S2, NIH_BMAP_M.S1. The subtracted library (NIH_BMAP_M.S3.1) was constructed as follows: PCR amplified cDNA inserts from NIH_BMAP_M.S2 clones from which 3' ESTs had been derived was used as a driver in a hybridization with the NIH_BMAP_M.S2 library in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (Life Technologies) to generate the NIH_BMAP_M.S3.1 library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)

TAG_TISSUE=olfactory bulbs
TAG_LIB=UI-M-BH2.1
TAG_SEQ=CATGG

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QY	411	GAGGACGCGTCCCGAGTGGTCCCAAGCCCTACTGGTTGAACCTATCTCGCATCGAG	470		
DB	617	GAGGACGCGTCCCGAGTGGTCCCAAGCCCTACTGGTTGAACCTATCTCGCATCGAG	558		
QY	471	CAGTTCGCAATCCCGGGGACGCTGTGGGGCGCGACGCGCGAGGCTTTATAGCCAC	530		
DB	557	CAGTTCGCAATCCCGGGGACGCTGTGGGGCGCGACGCGCGAGGCTTTATAGCCAC	498		
QY	531	CTCTTAGATCAGCTCTATGAACAAACGCTGCTCCCTCTACAGCGCGCGAGCGCTTG	590		
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QY	591	GGTGTCTCTTCTGCCCCCGTGAGATGGACCGCGCATGCACATCATCATCAACGGG	650		
DB	437	GGTGTCTCTTCTGCCCCCGTGAGATGGACCGCGCATGCACATCATCATCAACGGG	378		
QY	651	GAGGACATGGGCGCTAGCGCCCGGGGCTGCCAGTGTCTCAGCCCTCTACGCTGGTA	710		
DB	377	GAGGACATGGGCGCTAGCGCCCGGGGCTGCCAGTGTCTCAGCCCTCTACGCTGGTA	318		
QY	711	GATGTGTTGTTCTTCCACAAAGAGCGTGTGCTGCTCCAGCTGGAGTATGGCTTGCATCT	770		
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DB	257	CTGCAGACTCTGTGCGGACTAGTGATCCAGAGAGGGTGGTACACAGGCTGGCCATTGAT	198		
QY	831	GTGCTCCACCTGCGCAAGGACTTAAGGACTTCTGCAAGTACGATGACGATCAACGC	890		
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QY	951	AGTCTGAAGCTGGTCCGACAGCTCACAATCAGGCGCTGGAAATAAATAGACCGCATGTGA	1010		
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QY	1011	TGTTCTGAGAAAAAA 1027			
DB	17	AAAAAAAAAAAAAAAAA 1			
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BE650303					
LOCUS					
DEFINITION					
ACCESSION					
VERSION					
KEYWORDS					
SOURCE					
ORGANISM					
REFERENCE					
AUTHORS					
TITLE					
JOURNAL					
PUBMED					
COMMENT					

1011 TGTTCTGAGAAAAAA 1027
17 AAAAAAAAAAAAAAAAAA 1

BE650303 634 bp mRNA linear EST 06-SEP-2000
UI-M-BH2.1-apr-e-06-0-UI.r1 NIH_BMAP_M.S3.1 Mus musculus cDNA clone
UI-M-BH2.1-apr-e-06-0-UI.5', mRNA sequence.

BE650303
BE650303.1 GI:9976127
EST.
Mus musculus (house mouse)
Mus musculus
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 634)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
889548
Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
Email: mst@mail.nih.gov
cDNA Library Preparation: M.B. Soares Lab Clone distribution:
Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It
should be noted that Bento Soares is generating a small number of
additional specialized non-redundant arrays of BMAP cDNAs whose
collaborative arrangements
collaborative arrangements
Seq primer: M13 Reverse.
Location/Qualifiers
1. 634
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/db_xref="taxon:10090"
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/dev_stage="27-32 days"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; The
NIH_BMAP_M.S3.1 library is a subtracted library of a
series, ultimately derived from a mixture of individually
tagged normalized libraries from ten regions of the mouse
brain (cerebellum, brain stems, olfactory bulbs, pineal
hypothalamus, cortex, amygdala, basal ganglia, pineal
gland, striatum, hippocampus) after a series of
subtractions to reduce the representation of cDNAs from
which ESTs had already been generated. The following
serially subtracted libraries were generated in this
process: NIH_BMAP_M.S3.1, NIH_BMAP_M.S2, NIH_BMAP_M.S1.
The subtracted library (NIH_BMAP_M.S3.1) was constructed
as follows: PCR amplified cDNA inserts from NIH_BMAP_M.S2
clones from which 3' ESTs had been derived was used as a
driver in a hybridization with the NIH_BMAP_M.S2 library
in the form of single-stranded circles. The remaining
single-stranded circles (subtracted library) was purified
by hydroxyapatite column chromatography, converted to
double-stranded circles and electroporated into DH10B
bacteria (Life Technologies) to generate the
NIH_BMAP_M.S3.1 library. This procedure has been
previously described (Bonaldo, Lennon and Soares, Genome
Research 6:791-806, 1996)"

FEATURES					
SOURCE					

Query Match 61.0%; Score 632.4; DB 1; Length 634;
 Best Local Similarity 99.8%; Pred. No. 0.11; Indels 0; Gaps 0;
 Matches 633; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 137 AGGAACGGAGCCACACGCGTGGAGAGTTTCGCCACGCGTGTGTCTTCACTGAGCC 196
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Qy 197 CTTGGCCCGCCGCGCAGATTTCTAGTGGAAATTTAGAGAAAAGAGCTGGCGTGGCGG 256
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Qy 257 GCACCTACTGTTGGCCTGACCGCTCTGGATCCCGCAGTCTGGCCGCTGTACCCGAGTT 316
 Db 181 GCACCTACTGTTGGCCTGACCGCTCTGGATCCCGCAGTCTGGCCGCTGTACCCGAGTT 240

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 Db 241 TTCACTGCTGACTTGTGCTGAGCTTGGCCACAGTTGGGTCTTCGCTATCAGCCACCA 300

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Qy 437 AGCCCTACTGTTGAACCCCTATCTGCGCATCGAGCAGTTCGGAATCCCGGGACCGTCT 496
 Db 361 AGCCCTACTGTTGAACCCCTATCTGCGCATCGAGCAGTTCGGAATCCCGGGACCGTCT 420

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 Db 421 GGTGGCGCGACGCGCGCAGGCTTTATGACCACTCTTAGATCAGCTCTATGAACAAA 480

Qy 557 CGTGTGCTCTACAGCGCGCCAGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 616
 Db 481 CGTGTGCTCTACAGCGCGCCAGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540

Qy 617 TGGACCGCCGACATGCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 676
 Db 541 TGGACCGCCGACATGCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 600

Qy 677 GCTGCCAGTCTCTCAGCCCTCTACGCTGTGGTA 710
 Db 601 GCTGCCAGTCTCTCAGCCCTCTACGCTGTGGTA 634

RESULT 4
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 DEFINITION UI-M-BG2-bbm-a-08-0-UI.sl NIH BMAP MSC S1 Mus musculus cDNA clone
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 BE956589
 BE956589.1 GI:10601286
 EST.
 Mus musculus (house mouse)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.
 1 (bases 1 to 457)
 Bonaldo, M.F., Lennon, G. and Soares, M.B.
 Normalization and subtraction: two approaches to facilitate gene
 discovery
 Genome Res. 6 (9), 791-806 (1996)
 8889548
 CONTACT Contact: Chin, H
 National Institute of Mental Health
 6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
 20892-9643, USA
 Tel: 301 443 1706

Fax: 301 443 9890
 Email: mES@mail.nih.gov
 The sequence contained an oligo-dT track that was present in the
 oligonucleotide that was used to prime the synthesis of first
 strand cDNA and therefore this may represent a bonafide poly A
 tail. The sequence tag present in the cDNA between the NotI site
 and the oligo-dT track served to verify it as a clone from the
 olfactory bulb tissue cDNA Library Preparation: M.B. Soares Lab
 Clone distribution: Researchers may obtain BMAP cDNA clones from
 RESEARCH GENETICS. It should be noted that Bento Soares is
 generating a small number of additional specialized non-redundant
 arrays of BMAP cDNAs whose availability will be considered under
 appropriate and limited collaborative arrangements
 Seq primer: M13 Forward
 POLYA=Yes.

FEATURES
 source
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 /organism="Mus musculus"
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 /db_xref="taxon:10090"
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 NIH BMAP MSC S1 library is a subtracted library derived
 NIH BMAP MSC N. NIH BMAP MSC N was made from mouse spinal
 cord tissue. For a detailed description of the library
 from which this clone was derived, please visit our web
 site at brainest.eng.uiowa.edu.
 TAG_TISSUE=olfactory-bulbs
 TAG_LIB=NIH BMAP MSC_S1
 TAG_SEQ=CATCG"

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Qy 870 TAGCAATGAACGAATGAACCGCTGTCTGTGGCCACCAAGAGTCCCGGCTGGTGGCG 929
 Db 157 TAGCAATGAACGAATGAACCGCTGTCTGTGGCCACCAAGAGTCCCGGCTGGTGGCG 98

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RESULT 5
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 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Mus musculus (house mouse)
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 Sciurognathi; Muroidea; Muridae; Murinae; Mus.
 1 (bases 1 to 445)
 Okazaki, Y., Furuta, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
 Nishida, I., Osato, N., Saito, R., Suzuki, H., Yamashita, I.,
 Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
 Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C.,
 Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H.,
 Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V.,
 Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A.,
 Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T.,
 Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, T.,
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 Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M.,
 Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y.,
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 Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,
 Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S.,
 Rogers, J., Birney, E. and Hayashizaki, Y.
 Analysis of the mouse transcriptome based on functional annotation
 of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)
 1246681
 Contact: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic
 Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@gscc.riken.jp, URL: http://genome.gsc.riken.jp/
 Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,
 Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H.,
 Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R.,
 Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K.,
 Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and
 Hayashizaki, Y. Direct Submission
 Computational Analysis of Full-Length Mouse cDNAs Compared with
 Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new
 genes. Genome Res. 10 (10), 1617-1630 (2000)
 RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multicapillary sequencer. Genome Res.
 10 (11), 1757-1771 (2000)
 Computer-based methods for the mouse full-length cDNA
 encyclopedia: real-time sequence clustering for construction of a
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 cDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in RIKEN
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues.
 Tissues were provided by Michela Fagiolini and Takao K. Hensch (Laboratory for Neuroanal Circuit Development Brain Science Institute RIKEN 2-1 Hirose, Wako-shi, Saitama 351-0198 Japan) whose assistance we gratefully acknowledge. Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

FEATURES
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 QY 413 GGCAGCGTCCCGAGTGTGCTGGGAGAGGTCAACAGAGCCGA 472
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 Db 25 GTTCCGAATTCCTCCCGGAGCCGTCT 2

RESULT 6
 AW124138/c
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Mus musculus (house mouse)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.
 1 (bases 1 to 443)
 Ronaldo, M.F., Lennon, G. and Soares, M.B.
 Normalization and subtraction: two approaches to facilitate gene
 discovery
 Genome Res. 6 (9), 791-806 (1996)
 8889548

COMMENT

Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
Email: mEST@mail.nih.gov

The sequence contained an oligo-dr track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dr track served to identify it as a clone from the normalized olfactory bulbs library cDNA Library Preparation: M.B. Soares Lab Clone distribution: NIH BMAP cDNA clones will be made available by the means that is soon to be determined. When NIH determines the means for distribution of the BMAP cDNA clones, this record will be updated accordingly when that means is determined.
Seq primer: M13 Forward
POLYA=Yes.

FEATURES

Source

1. 443
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UI-M-BH2.1-apr-e-06-0-UI"
/dev_stage="27-32 days"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NIH BMAP M_S3.1"
/note="Vector: p77T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI: The NIH_BMAP_M_S3.1 library is a subtracted library of a series, ultimately derived from a mixture of individually tagged normalized libraries from ten regions of the mouse brain (cerebellum, brain stems, olfactory bulbs, hypothalamus, cortex, amygdala, basal ganglia, pineal gland, striatum, hippocampus) after a series of subtractions to reduce the representation of cDNAs from which ESTs had already been generated. The following serially subtracted libraries were generated in this process: NIH_BMAP_M_S3.1, NIH_BMAP_M_S2, NIH_BMAP_M_S1. The subtracted library (NIH_BMAP_M_S3.1) was constructed as follows: PCR amplified cDNA inserts from NIH_BMAP_M_S2 clones from which 3' ESTs had been derived was used as a driver in a hybridization with the NIH_BMAP_M_S2 library in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (Life Technologies) to generate the NIH_BMAP_M_S3.1 library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)
TAG_TISSUE=olfactory-bulbs
TAG_LIB=NIH_BMAP_M_S3.1
TAG_SEQ=CATGG"

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704 TGTGGTAGATGTTGTTGCTTCACCAAGAGCGTGCCTGTCAGCTGGAGTATGCGCTT 763
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RESULT 7

BY267664/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

COMMENT

BY267664 402 bp mRNA linear EST 11-DEC-2002
CDNA clone K430018111 5', mRNA sequence.

BY267664
BY267664.1 GI:26457871

EST.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

1 (bases 1 to 402)

Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojohori, T., Baldarelli, R., Hill, D. P., Bult, C., Hume, D. A., Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K. W., Blake, J. A., Bradt, D., Brusci, V., Chothia, C., Corbani, L. E., Cousins, S., Dalla, E., Dragan, T. A., Fletcher, C. P., Forrest, A., Frazer, K. S., Gaasterland, T., Gariboldi, M., Gissi, C., Godik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I. J., Jarvis, E. D., Kanai, A., Kawai, H., Kawasawa, Y., Kedzierski, R. M., King, B. D., Konagaya, A., Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons, P. A., Maglott, D. R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W. J., Pertea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Ramachandran, S., Ravasi, F., Reed, J. C., Reed, D. J., Reid, J., Ring, B. Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C. A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tomita, M., Veraturo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L. G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S., Rogers, J., Birney, E. and Hayashizaki, Y.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
12466851
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216

Email: genome-res@gsr.riken.jp, URL: <http://genome.gsc.riken.jp/>
 Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission
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 Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
 RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
 Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
 Tissues were provided by Michela Fagioli and Takao K. Hensch (Laboratory for Neuronal Circuit Development Brain Science Institute RIKEN 2-1 Hirosawa Wako-shi, Saitama 351-0198 Japan) whose assistance we gratefully acknowledge. Please visit our web site (<http://genome.gsc.riken.go.jp/>) for further details.
 Location/Qualifiers

FEATURES

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1. 402
    /organism="Mus musculus"
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Matches 400; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Oy 212  GGTATTTCTAGTGGAATTTGAGGAAAAGAGCTGGGCTGGTCCGGGACCTACGCTTTGG 271
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Oy 342  GGTATTTCTAGTGGAATTTGAGGAAAAGAGCTGGGCTGGTCCGGGACCTACGCTTTGG 283
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RESULT 8
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 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 PUBMED
 COMMENT

BY105284 384 bp mRNA linear EST 07-DEC-2002
 BY105284 RIKEN full-length enriched, pooled tissues, adult spleen,
 etc. Mus musculus cDNA clone K630160C04 5', mRNA sequence.
 BY105284
 BY105284.1 GI:26215901
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 Mus musculus (house mouse)
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 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.
 1 (bases 1 to 384)
 Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
 Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I.,
 Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
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 Wells, C., Wilming, L. G., Wyshew-Boris, A., Yanagisawa, M., Yang, I.,
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 Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M.,
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 Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,
 Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S.,
 Rogers, J., Birney, E. and Hayashizaki, Y.
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 Nature 420, 563-573 (2002)
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 Laboratory for Genome Exploration Research Group, RIKEN Genomic
 Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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 Fax: 81-45-503-9216
 Email: genome-res@gsr.riken.jp, URL: <http://genome.gsc.riken.jp/>
 Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,
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 Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K.,
 Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and
 Hayashizaki, Y. Direct Submission
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 cDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in RIKEN
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues.

Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

FEATURES		REFERENCE	
source		AUTHORS	
Location/Qualifiers			
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Qy	181	GCTTCAGTCTGAGCCCTCGCCCGCCAGGATTTCTAGTGGAAATTGAGGAAAAG	240
Db	194	GCTTCAGTCTGAGCCCTCGCCCGCCAGGATTTCTAGTGGAAATTGAGGAAAAG	253
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Db	314	CCGCTGTACCCGAGTTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	373
Qy	361	CTATCACACGC 371	
Db	374	CTATCACACGC 384	
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DEFINITION		BY670130 RIKEN full-length enriched, 14.5 days embryo df/df	
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ACCESSION		BY670130	
VERSION		BY670130.1	
KEYWORDS		EST.	
SOURCE		Mus musculus (house mouse)	
ORGANISM		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

1. (bases 1 to 376)

Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C., Hume, D. A., Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K. W., Blake, J. A., Bradt, D., Bruscia, V., Ciothia, C., Corbani, L. E., Cousins, S., Dalla, E., Drganci, T. A., Fletcher, C. F., Forrest, A., Frazer, K. S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hitokawa, N., Jackson, I. J., Jarvis, E. D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R. M., King, B. L., Konagaya, A., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagasawa, T., Numata, K., Okido, T., Pavan, W. J., Pertea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J. C., Reed, D. J., Reid, J., Ring, B. Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C. A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L. G., Wyshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, F., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shingawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S., Rogers, J., Birney, E. and Hayashizaki, Y.

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12466851

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Email: genome-res@gsr.riken.jp, URL: <http://genome.gsc.riken.jp/>

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cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Tissues were provided by Michelle Brinkmeier and Sally Camper (Dept. Human Genetics University of Michigan Medical School 4301 MSRB 3 1500 W. Medical Center Dr. Ann Arbor, MI 48109-0638 USA) whose assistance we gratefully acknowledge.

Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

Location/Qualifiers

1. .376

/organism="Mus musculus"

FEATURES

Source

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/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="K820011E02"
/tissue_type="Rathke's pouches"
/dev_stage="14.5 days embryo df/df"
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df/df Rathke's pouches"

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Matches 370; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

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Qy 707 GGTAGATGTGTTTCTTCCACCAAGAGCGTGCCTGCTCAGCTGAGTATGCTTGGCC 766
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RESULT 10
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ACCESSION AW125078
VERSION AW125078.1 GI:6100608
KEYWORDS EST.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
1 (bases 1 to 336)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
8889548
Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
Email: mEST@mail.nih.gov
The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. The sequence tag present in the cDNA between the NotI site
and the oligo-dT track served to identify it as a clone from the
normalized prefrontal cortex library cDNA Library Preparation: M.B.

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Soares Lab Clone distribution: NIH BMAP cDNA clones will be made available by the means that is soon to be determined. When NIH determines the means for distribution of the BMAP cDNA clones, this record will be updated accordingly when that means is determined.

Seq primer: M13 Forward

POLYA=yes.

Location/Qualifiers

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tagged (cerebellum, brain stems, olfactory bulbs,
hypothalamus, cortex, amygdala, basal ganglia, pineal
gland, striatum, hippocampus) after a series of
subtractions to reduce the representation of cDNAs from
which ESTs had already been generated. The following
serially subtracted libraries were generated in this
process: NIH_BMAP_M.S3.1, NIH_BMAP_M.S2, NIH_BMAP_M.S1.
The subtracted library (NIH_BMAP_M.S3.1) was constructed
as follows: PCR amplified cDNA inserts from NIH_BMAP_M.S2
clones from which 3' ESTs had been derived was used as a
driver in a hybridization with the NIH_BMAP_M.S2 library
in the form of single-stranded circles. The remaining
single-stranded circles (subtracted library) was purified
by hydroxyapatite column chromatography, converted to
double-stranded circles and electroporated into DH10B
bacteria (Life Technologies) to generate the
NIH_BMAP_M.S3.1 library. This procedure has been
previously described (Bonaldo, Lennon and Soares, Genome
Research 6:791-806, 1996)
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TAG_SEQ=GCNCA"

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Best Local Similarity 99.7%; Pred. No. 3.5;
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Qy 699 TACGCTGTGTGATGTGTTTGTCCACCAAGAGCGTGGTCTGGTCCAGCTGAGTAT 758
Db 336 TACGCTGTGTGATGTGTTTGTCCACCAAGAGCGTGGTCTGGTCCAGCTGAGTAT 277

Qy 759 GGCTTGCCATCTGCGAGACTCTGCGGACTAGTATCCAGAGAGGGTGTACACAGG 818
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Qy 819 CTGGCCATTGATGTCTCCACTGCCCAAGAGCTTGAAGGACTTCTGCAAGTACGAATGA 878
Db 216 CTGGCCATTGATGTCTCCACTGCCCAAGAGCTTGAAGGACTTCTGCAAGTACGAATGA 157

Qy 879 ACGAATGAACGCTGTCTGTGGCCACAGAGCAAAAGTCCCGGTGGTGGCCCTCCCTCT 938
Db 156 ACGAATGAACGCTGTCTGTGGCCACAGAGCAAAAGTCCCGGTGGTGGCCCTCCCTCT 97

Qy 939 AGAGAAGTGGCTGTGTAAGCTGTCCAGCTCACAATCAGGCTGGGAATAAATAG 998
Db 96 AGAGAAGTGGCTGTGTAAGCTGTCCAGCTCACAATCAGGCTGGGAATAAATAG 37

Qy 999 AGCCGATGTGATGTCTTGAGAAAAAAGAAAAA 1034
Db 36 AGCCGATGTGATGTCTTGAGAAAAAAGAAAAA 1

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QY 766 CATCTGCGAGCTCTGTGCGGACTAGTATCCAGAGAGGGTGGTACACAGGCTGSCCA 825
Db 4 CCTCTCTGCGAGCTCTGTGCGGACTAGTATCCAGAGAGGGTGGTACACAGGCTGSCCA 63
QY 826 TTGATGTGCTCCACTGCCCAAGGACTGAAGGACTTCTGCAAGTACGAATGAACGAATG 885
Db 64 TTGATGTGCTCCACTGCCCAAGGACTGAAGGACTTCTGCAAGTACGAATGAACGAATG 123
QY 886 AACGCTGTCTGTGGCCACAGAGCAAAAGTCCCGGTGGTGGCCCTCTAGAGAAG 945
Db 124 AACGCTGTCTGTGGCCACAGAGCAAAAGTCCCGGTGGTGGCCCTCTAGAGAAG 183
QY 946 TGGCTAGTCTGAAGCTGTGCGCAGCTCAATCAGGCGTGGAAATAAATAGAGCCGAT 1005
Db 184 TGGCTAGTCTGAAGCTGTGCGCAGCTCAATCAGGCGTGGAAATAAATAGAGCCGAT 243
QY 1006 GTGGATGTTCTGA 1018
Db 244 GTGGATGTTCTGA 256

RESULT 15
CG479214
LOCUS 251 bp mRNA linear GSS 01-OCT-2003
DEFINITION OST9837 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST9837, mRNA
sequence.
ACCESSION CG479214
VERSION CG479214.1 GI:37230103
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 251)
AUTHORS Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J.,
Piggott, J., BeltrandelRio, H., Buxton, E.C., Edwards, J., Finch, R.A.,
Fridde, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaing, C.,
Key, B.W. Jr., Kipp, P., Kohlhauff, B., Ma, Z.-Q., Markesich, D.,
Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z.,
Sparks, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N.,
Zhu, Q., Person, C. and Sands, A.T.
Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
screen to identify potential targets for therapeutic intervention
Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
14610273
CONTACT: Zambrowicz BP
OmiBank
Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com
Gene trap sequence tag generated by 3' RACE from mouse ES cells as
described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
Class: Gene Trap.
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Location/Qualifiers
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Best Local Similarity 99.2%; Pred. No. 11;
Matches 245; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 766 CATCTGCGAGCTCTGTGCGGACTAGTATCCAGAGAGGGTGGTACACAGGCTGSCCA 825
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QY 886 AACGCTGTCTGTGGCCACAGAGCAAAAGTCCCGGTGGTGGCCCTCTAGAGAAG 945
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QY 946 TGGCTAGTCTGAAGCTGTGCGCAGCTCAATCAGGCGTGGAAATAAATAGAGCCGAT 1005
Db 185 TGGCTAGTCTGAAGCTGTGCGCAGCTCAATCAGGCGTGGAAATAAATAGAGCCGAT 244
QY 1006 GTGGATG 1012
Db 245 GTGGATG 251

RESULT 16
BX632311/c
LOCUS 228 bp mRNA linear EST 12-AUG-2003
DEFINITION BX632311 pBluescript Lion Mus musculus cDNA clone LIONp462C0276 3',
mRNA sequence.
ACCESSION BX632311
VERSION BX632311.1 GI:33612186
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 228)
AUTHORS Henrich, J., Hermanns, J., Kranz, H., Loebbert, R., Schluter, T.,
Schuette, D., Weindel, M., Heil, O., Ebert, L., Neubert, P., Peters, M.,
Radelof, J., Schneider, D. and Korn, B.
Mouse ArrayTAG cDNA (LION)
Unpublished (2003)
CONTACT: Ina Rolf
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD; LIONp462C0276.
RZPDLIB;
Mouse ArrayTAG cDNA (LION)
http://www.rzpd.de/cgi-bin/products/showLib.pl.cgi/response?libNo=4
62 Contact: Ina Rolf
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 111
www.rzpd.de
This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seq primer:
RP: CAGGAACAGCTATGAC.
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Location/Qualifiers
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Db 228 GACTAGTATCCAGAGAGGGTGGTACACAGGCTGGCCATTGATGTCTCCACTGCCCA 169
QY 847 AAGGACTGAAGGACTTCTGCAAGTACGAATGAACGCTGTCTGTGCGCCACCA 906
Db 168 AAGGACTGAAGGACTTCTGCAAGTACGAATGAACGCTGTCTGTGCGCCACCA 109
QY 907 GAGCAAAAGTCCCGGTGGTGGCCCTCGCTCTAGAGAAAGTGGCTAGTCTGAAGCTGCTCG 966

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Thu Mar 2 10:54:22 2006

Db 108 GAGCAAGTCCCGTGGTGGCGCTGCTCTAGAGAGTGGCTAGTCTGAAGCTGGTCG 49
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Db 48 CACAGCTCACATCAGGCTGGAATAATAATAGAGCCGATGGGA 5

RESULT 17
CX214893/c
LOCUS
DEFINITION MNS23392 Mouse Neurosphere Normalized cDNA library Mus musculus
CDNA 5', mRNA sequence. EST 29-DEC-2004

ACCESSION CX214893
VERSION CX214893
KEYWORDS CX214893.1 GI:56870185
SOURCE EST.

ORGANISM Mus musculus (house mouse)
Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE 1 (Bases 1 to 200)
AUTHORS Williams, C., Wirta, V., Lundberg, J. and Frisen, J.
TITLE Expressed sequence tags of cDNA clones from murine neurospheres
JOURNAL Unpublished (2005)
COMMENT Contact: Williams, C.
Molecular Biotechnology
Institution of Biotechnology
Albano University Center, KTH-Royal Institute of Technology, 106
91 Stockholm, Sweden
Tel: +46855378332
Fax: +46855378481
Email: cecilia.williams@biotech.kth.se
Seq primer: M13REV.

FEATURES
Location/Qualifiers
1..200
/organism="Mus musculus"
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/strain="C57BL/6"
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/sex="MALE"
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/clone_lib="Mouse Neurosphere Normalized cDNA library"
/note="Organ: Adult brain; Vector: pCMVSPORT6.0; A cDNA library was constructed in pCMVSPORT6.0 from RNA isolated from neurospheres of adult male and female mice. Custom normalized cDNA library by Invitrogen/ResGen"

Query Match 19.2%; Score 199; DB 1; Length 200;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 380 CCGTGTGCCCCGGGAGGTCAACAGAGCGGAGCGGTCGCCAGTGGTCCCAAGC 439
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Qy 440 CCTACTGTGTGAACCTATCTCGCATCGAGCAGTTCGGAATTCGCCGGACCGTCTGT 499
Db 139 CCTACTGTGTGAACCTATCTCGCATCGAGCAGTTCGGAATTCGCCGGACCGTCTGT 80

Qy 500 GGGCCGACGCGCGCAGGCTTTATAGCCACCTCTTAGATCAGCTCTATGAACAAAGT 559
Db 79 GGGCCGACGCGCGCAGGCTTTATAGCCACCTCTTAGATCAGCTCTATGAACAAAGT 20

Qy 560 GCTGCTCTCTACAGCGGC 578
Db 19 GCTGCTCTCTACAGCGGC 1

RESULT 18
AV022299

LOCUS
DEFINITION AV022299 Mus musculus 18-day embryo C57BL/6J Mus musculus cDNA
clone 1190026D24, mRNA sequence. EST 28-AUG-1999

ACCESSION AV022299
VERSION AV022299.1 GI:4799291
KEYWORDS EST.
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE 1 (Bases 1 to 195)
AUTHORS Carninci, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, K., Akahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T., Hara, A., Hayatsu, N., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Kawai, J., Kikuchi, N., Kojima, Y., Matsuyama, T., Naitsumu, H., Oda, H., Owa, C., Sato, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Suganara, Y., Suzuki, H., Suzuki, H., Tateno, M., Tomaru, Y., Tomihata, N., Watanabe, S., Yagame, M., Yamamura, T., Yokota, T., Yoshino, M., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.

RIKEN Mouse ESTs
Unpublished (1999)
Contact: Chie Owa
Genome Science Laboratory
RIKEN
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-9145
Fax: 81-298-36-9098
Email: genome-res@rtc.riken.go.jp

Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for further details.

FEATURES
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/mol_type="mRNA"
/strain="C57BL/6J"
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Matches 191; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy 883 ATGAACGCTCTGTGTGGCCACAGAGCAAAAGTCCCGGTGGTGGCCCTCTAGAG 942
Db 61 ATGAACGCTCTGTGTGGCCACAGAGCAAAAGTCCCGGTGGTGGCCCTCTAGAG 120

Qy 943 AAGTGGCTAGTCTGAAGCTGTGTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCT 1002
Db 121 AAGTGGCTAGTCTGAAGCTGTGTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCT 180

Qy 1003 GATGGATGTTCTG 1017
Db 181 GATGGATGTTCTG 195

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Job time : 5 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 2, 2006, 10:54:58 ; Search time 1 Seconds
(without alignments)
3.181 Million cell updates/sec

Title: US-10-014-774-1
Perfect score: 1036
Sequence: 1 cctgttgacggcttgag.....gagaaaaa.....gagaaaaa 1036

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 2 seqs, 1535 residues

Total number of hits satisfying chosen parameters: 4

Minimum DB seq length: 10
Maximum DB seq length: 1036

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 2 summaries

Database : us-10-014-774-1.sl.rng4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1036	100.0	1036	1 AAA89043	Murine muscle-spec
2	487.5	47.1	499	1 AAA89047	Mouse muscle-spec

ALIGNMENTS

RESULT 1
AAA89043
ID AAA89043 standard; cDNA; 1036 BP.
XX AC AAA89043;
XX 05-MAR-2001 (first entry)
XX DE Murine muscle-specific protein Ozz cDNA.
XX Ozz; mouse; muscle-specific protein; myogenesis; muscle damage;
KW galactosialidosis; myocardial infarction; angina; therapy; diagnosis; ss.
XX Mus sp.
XX Key Location/Qualifiers
XX CDS 21..878 /*tag= a
XX FT
XX WO200066733-A1.
XX 09-NOV-2000.
XX 28-APR-2000; 2000WO-US011900.
XX 29-APR-1999; 99US-013181P.
PR

XX (STUD-) ST JUDE CHILDREN'S RES HOSPITAL.
XX D'azzo A, Bongiovanni A, Nastasi T;
XX WPI; 2001-007221/01.
XX P-PSDB; AAB19850.
XX Novel protein Ozz and nucleic acid encoding the protein involved in
XX development and function of muscle, useful as target for identifying
XX drugs effective in treating myogenesis disorders.
XX Claim 6; Fig 2A; 62pp; English.
XX The present sequence is that of cDNA encoding a novel murine muscle-
XX specific protein, termed Ozz (see AAB19850), that regulates development
XX and function of muscle cells. The Ozz gene was identified overlapping
XX exon 1a of the murine PPCA gene, transcribed on the opposite strand. The
XX corresponding cDNA was isolated from a mouse heart library. It shows 85%
XX homology to human Ozz cDNA (see AAB9044). The murine Ozz protein is
XX preferentially expressed by a 1.0 kb mRNA in heart and skeletal muscle.
XX This protein shares homology with neuralised proteins, associated with a
XX number of muscle proteins, including beta-catenin. Ozz protein is useful
XX for detecting damage to muscle tissue or disease associated with a defect
XX in Ozz expression. Increase in the level of Ozz protein in blood or in a
XX blood fraction indicates damage to muscle tissue in the heart and an
XX abnormal level or localization of Ozz in muscle cells from the atrium of
XX the heart of a subject is useful for detecting galactosialidosis
XX (claimed). The presence of Ozz in blood or a blood fraction indicates
XX muscle tissue damage e.g. ischaemia associated with either unstable
XX angina, myocardial infarction or both. Nucleotide sequences derived from
XX the gene encoding Ozz and peptide sequences derived from Ozz are useful
XX as targets to identify drugs that are effective in treating myogenesis
XX disorders
XX Sequence 1036 BP; 215 A; 321 C; 297 G; 203 T; 0 U; 0 Other;

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Matches 1036;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
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QY 61	GGAGCCCTGCGCGCCAGAGCCCTCCACCCGCTCCACCAAGTCATGGAGCAACA	120		
DB 61	GGAGCCCTGCGCGCCAGAGCCCTCCACCCGCTCCACCAAGTCATGGAGCAACA	120		
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DB 121	TCCGCATGACCCCTCAGGAACGGAGCCACACGCGTGGAGAGTTTCGCCACCGTGTGT	180		
QY 181	GCTTCAGTGTGAGCCCTCGGCCCTCGGCCAGGATATTTCTAGTGAATTTGAGGAAAAG	240		
DB 181	GCTTCAGTGTGAGCCCTCGGCCCTCGGCCAGGATATTTCTAGTGAATTTGAGGAAAAG	240		
QY 241	AGCTGGGTGTGGGGGACCTTACCTGTGGCTGACCGCTCTGATCCCGCAGTCTGG	300		
DB 241	AGCTGGGTGTGGGGGACCTTACCTGTGGCTGACCGCTCTGATCCCGCAGTCTGG	300		
QY 301	CCGCTGTACCCGAGTTTTTCACTGTGCTGCTTGGTTCAGCTTGGCCACAGTGGGTCTTCG	360		
DB 301	CCGCTGTACCCGAGTTTTTCACTGTGCTGCTTGGTTCAGCTTGGCCACAGTGGGTCTTCG	360		
QY 361	CTATCACACGCCACCAACCCGTGTGGCCCGGGAAGGTCAACACAGAGCGGAGCGG	420		
DB 361	CTATCACACGCCACCAACCCGTGTGGCCCGGGAAGGTCAACACAGAGCGGAGCGG	420		
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DB 421	TCCCCAGTGGTCCCCAAGCCCTTACTGGTTGAACCTATCTGGCATCGGACGATTCGGA	480		

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Job time : 1 secs

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Sequence 14: Appl

ALIGNMENTS

RESULT 1

TITLE OF INVENTION: Protein Specific for Cardiac and Skeletal Muscle

FILE REFERENCE: 242 / 11303 001
CURRENT IDENTIFICATION NUMBER: IIS / 10 / 014 774

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;
: PRIOR FILING DATE: 1999-04-29

: SEO ID NO 1

: TYPE: DNA

US-10-014-774-1

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Query Match      100.0%; Score 1036; DB 1; Length 1036;
Best Local Similarity 100.0%; Pred. No. 6.9e-12;
Matches 1036; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1 CCTGTTGCA CGGCTTGGAGATGGCTGCTCCCTCCGAACACGTAGGACTGGGTGCCCCAC 60

1	CCCTGTTGCAGGGCTTGGAGATGGCTGCTCCCTCCGAACACAGTAGACTGGGTGCCCCAC	60
61	GGAGCCCTGGGGCCCCAGAGCCCTCCACCCGCTTCCACCAAGTCATGGAGGCCAACA	120
61	GGAGCCCTGGGGCCCCAGAGCCCTCCACCCGCTTCCACCAAGTCATGGAGGCCAACA	120
121	TCGCGATGACCCCTCAGGAACCGGAGCCACACGCGTGGAGAGTTTCGCCCCACGGTGCT	180
121	TCGCGATGACCCCTCAGGNAACGGAGCCACACGCGTGGAGAGTTTCGCCCCACGGTGCT	180
181	GCTTCAGTCGTGAGCCCTGGGCCCGCGGCCAGGTAATTTCTAGTGGAAATTTGAGGAAAAG	240
181	GCTTCAGTCGTGAGCCCTGGGCCCGCGGCCAGGTAATTTCTAGTGGAAATTTGAGGAAAAG	240
241	AGCTGGGCTGGTGGGGGCACTACGCTTCCTGGCCCTCAGCGCTCTGGATCCCGCCAGTCTGG	300
241	AGCTGGGCTGGTGGGGGCACTACGCTTCCTGGCCCTCAGCGCTCTGGATCCCGCCAGTCTGG	300
301	CCGCTGTACCCGAGTTTTTCATCGCTGACATTGGTTCAGCCTTGGCCACAGTTGGGTCCTCG	360
301	CCGCTGTACCCGAGTTTTTCATCGCTGACATTGGTTCAGCCTTGGCCACAGTTGGGTCCTCG	360
361	CTATCACACGCCACCAACCCGTGTGCCCGGGNAGGTCACACAGAGCGGAGGCAGCGG	420
361	CTATCACACGCCACCAACCCGTGTGCCCGGGNAGGTCACACAGAGCGGAGGCAGCGG	420
421	TCGCCAGTGTGCCAAGCCCTACTGTTGAAACCTATCTGCGCATCGAGCAGTTCGGAA	480
421	TCGCCAGTGTGCCAAGCCCTACTGTTGNAACCTATCTGCGCATCGAGCAGTTCGGAA	480
481	TTCCCGGGACCGTCTGGTGGGGCGCAGCGGCCAGGGCTTTATAGCCACCTCTTAGATC	540
481	TTCCCGGGACCGTCTGGTGGGGCGCAGCGGCCAGGGCTTTATAGCCACCTCTTAGATC	540
541	AGCTCTATGACAAACGCTGCTGCTCCTCCTACAGCGCCGAGCCGCTTGGGTCTCTCT	600

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Db      541  AGCTCTATGAACAAAACGCTGTGCTCTCTACAGCGCGCCGAAAGCGCTTGGGTCTCT 600
Qy      601  TCTGCCCGCTGAGATGGGACCCCGACATGACATCATCATCAACGGGGAGACATGG 660
Db      601  TCTGCCCGCTGAGATGGGACCCCGACATGACATCATCATCAACGGGGAGACATGG 660
Qy      661  GCGCTAGCGCCCGGGGCTGCGAGCTGCTCAGCCCTCTACGCTGTGCTAGATGTGTTG 720
Db      661  GCGCTAGCGCCCGGGGCTGCGAGCTGCTCAGCCCTCTACGCTGTGCTAGATGTGTTG 720
Qy      721  CTTCCACAAGAGCGTGTGCTGTGCTGAGTGTGCTGAGTGTGCTGAGTGTGCTGAG 780
Db      721  CTTCCACAAGAGCGTGTGCTGTGCTGAGTGTGCTGAGTGTGCTGAGTGTGCTGAG 780
Qy      781  TGTGCCAGTGTGATCCAGAGAGGTGTGTAACAGGCTGGCCATTCATGATGTGCTCAC 840
Db      781  TGTGCCAGTGTGATCCAGAGAGGTGTGTAACAGGCTGGCCATTCATGATGTGCTCAC 840
Qy      841  TGCCCAAGGACTCAAGGACTTCTGCAAGTACGAATGAACGAATGAACGCTGTCTGTGG 900
Db      841  TGCCCAAGGACTCAAGGACTTCTGCAAGTACGAATGAACGAATGAACGCTGTCTGTGG 900
Qy      901  CCACGAGCAAGTCTCCCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGAG 960
Db      901  CCACGAGCAAGTCTCCCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGAG 960
Qy      961  TGGTGGACAGCTCACATCAGGCTGGAATGAATGAATGAATGAATGAATGAATGAATGA 1020
Db      961  TGGTGGACAGCTCACATCAGGCTGGAATGAATGAATGAATGAATGAATGAATGAATGA 1020
Qy      1021  AAAAAAAAAAAAAA 1036
Db      1021  AAAAAAAAAAAAAA 1036

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RESULT 2
US-10-014-774-14/c
; Sequence 14, Application US/10014774
; Publication No. US20020099173A1
; GENERAL INFORMATION:
; APPLICANT: D'Azzo, Alessandra
; APPLICANT: Nastasi, Tommaso
; TITLE OF INVENTION: Protein Specific for Cardiac and Skeletal Muscle
; FILE REFERENCE: 2427/1F509-US1
; CURRENT APPLICATION NUMBER: US/10/014, 774
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: PCT/US00/11900
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/131,814
; PRIOR FILING DATE: 1999-04-29
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 499
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-014-774-14

Query Match      47.1%; Score 487.5; DB 1; Length 499;
Best Local Similarity 99.8%; Pred. No. 1.9e-05;
Matches 498; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy      265  GTCTTGGCTGACCGCTCTGGATCCCGCAGTCTGGCGCTGTACCCGAGTTTCACTGC 324
Db      499  GTCTTGGCTGACCGCTCTGGATCCCGCAGTCTGGCGCTGTACCCGAGTTTCACTGC 440
Qy      325  CTGACTTGGTCTGAGCTTGGCCACAGTTGGTCTTGGCTATCACAGCCACCAACCGTG 384
Db      439  CTGACTTGGTCTGAGCTTGGCCACAGTTGGTCTTGGCTATCACAGCCACCAACCGTG 380
Qy      385  TGCCCGGGAGGTCACACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 444

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Db      379  TGCCCGGGAAAGGTCAACACAGAGCGAGCGGTCCCGAGTGGTCCCAAGCCCTAC 320
Qy      445  TGCTTGAACCCCTATCTCGGCATCGAGCAGTTCGGAATTCGCCGGGACCGTCTGGTGGCC 504
Db      319  TGCTTGAACCCCTATCTCGGCATCGAGCAGTTCGGAATTCGCCGGGACCGTCTGGTGGCC 260
Qy      505  GCAGCGCGCCAGCGCTTTATAGCCACTCTTAGATCAGCTCTATGAACAAAAAGTGTGTC 564
Db      259  GCAGCGCGCCAGCGCTTTATAGCCACTCTTAGATCAGCTCTATGAACAAAAAGTGTGTC 200
Qy      565  CTCTACAGCGCCGAGCGCTTGGGTGTCTTCTTGTGCCCCGTGAGGATGGGACCG 624
Db      199  CTCTACAGCGCGCCGAGCGCTTGGGTGTCTTCTTGTGCCCCGTGAGGATGGGACCG 140
Qy      625  CCACATGACATCATCATCAACGGGAGGACATGGGCGCTTAGCGCCCGGGGCTGCCAG 684
Db      139  CCACATGACATCATCATCAACGGGAGGACATGGGCGCTTAGCGCCCGGGGCTGCCAG 80
Qy      685  CTCTCAGCGCCCTCTACGCTGTGATAGTGTGTTGTTCTTCCACCAAGAGCGT-GCGTCTG 743
Db      79  CTCTCAGCGCCCTCTACGCTGTGATAGTGTGTTGTTCTTCCACCAAGAGCGTGTGCGCTG 20
Qy      744  GTCCAGCTGGAGTATGCT 762
Db      19  GTCCAGCTGGAGTATGCT 1

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RESULT 3
US-10-719-900-53916
; Sequence 53916, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719, 900
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 53916
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-53916

Query Match      2.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      581  AAGCCGCTGGGTGTTCTCTCTTCG 605
Db      1  AAGCCGCTGGGTGTTCTCTCTTCG 25

RESULT 4
US-10-719-900-162890
; Sequence 162890, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719, 900
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 162890
; LENGTH: 25
; TYPE: DNA

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; ORGANISM: Mus musculus
US-10-719-900-162890

Query Match          2.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 710 AGATGCTTTGCTTCCACCAAGAGC 734
    |||||
Db 1 AGATGCTTTGCTTCCACCAAGAGC 25

RESULT 5
US-10-719-900-266177
; Sequence 266177, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 266177
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-266177

Query Match          2.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 616 ATGGACCGCGGACATGCACATCAT 640
    |||||
Db 1 ATGGACCGCGGACATGCACATCAT 25

RESULT 6
US-10-719-900-297068
; Sequence 297068, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 297068
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-297068

Query Match          2.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 728 CAAGACGCTGCTCTGCTCCAGCTG 752
    |||||
Db 1 CAAGACGCTGCTCTGCTCCAGCTG 25

RESULT 7
US-10-719-900-685399
; Sequence 685399, Application US/10719900

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; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 685399
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-685399

Query Match          2.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 744 GTCCAGCTGGAGTATGGCTTGCCAT 768
    |||||
Db 1 GTCCAGCTGGAGTATGGCTTGCCAT 25

RESULT 8
US-10-719-900-705299
; Sequence 705299, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 705299
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-705299

Query Match          2.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 924 GTGGCCCTGCTCTAGAGAGTGG 948
    |||||
Db 1 GTGGCCCTGCTCTAGAGAGTGG 25

RESULT 9
US-10-719-900-843156
; Sequence 843156, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 843156
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus

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US-10-719-900-843156

Query Match 2.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 876 TGAACGAATCAAGCCCTGCTGTGG 900
|||||
Db 1 TGAACGAATCAAGCCCTGCTGTGG 25

RESULT 10

US-10-719-900-870471
; Sequence 870471, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 870471
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-870471

Query Match 2.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 460 TGGCATCGAGCAGTTCGGAATCC 484
|||||
Db 1 TGGCATCGAGCAGTTCGGAATCC 25

RESULT 11

US-10-719-900-886835
; Sequence 886835, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 886835
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-886835

Query Match 2.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 946 TGGCTAGTCTGAAGCTGCTGCACA 970
|||||
Db 1 TGGCTAGTCTGAAGCTGCTGCACA 25

RESULT 12

US-10-719-900-894080
; Sequence 894080, Application US/10719900
; Publication No. US20050026164A1

GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 894080
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-894080

Query Match 2.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 961 TGGTCGACAGCTCACAATCAGGC 985
|||||
Db 1 TGGTCGACAGCTCACAATCAGGC 25

RESULT 13

US-10-719-900-896569
; Sequence 896569, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 896569
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-896569

Query Match 2.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 445 TGGTTGAACCTATCTGCGCATCGA 469
|||||
Db 1 TGGTTGAACCTATCTGCGCATCGA 25

RESULT 14

US-11-036-317-85479/c
; Sequence 85479, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 85479
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus

US-11-036-317-85479

Query Match 2.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 437 AGCCCTACTGGTTGAACCCCTATCTG 461
Db 25 AGCCCTACTGGTTGAACCCCTATCTG 1

RESULT 15

US-11-036-317-99886/c
; Sequence 99886, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 99886
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-99886

Query Match 2.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 335 CAGCCTTGGCCACAGTGGGCTTC 359
Db 25 CAGCCTTGGCCACAGTGGGCTTC 1

RESULT 16

US-11-036-317-117157/c
; Sequence 117157, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 117157
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-117157

Query Match 2.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 460 TCGCATCGAGCAGTTCGGAATTC 484
Db 25 TCGCATCGAGCAGTTCGGAATTC 1

RESULT 17

US-11-036-317-118199/c

; Sequence 118199, Application US/11036317
; Publication No. US20050214823A1

; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 118199
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus

US-11-036-317-118199

Query Match 2.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 265 GTCTGGCCTGACGGCTCTGGATCC 289
Db 25 GTCTGGCCTGACGGCTCTGGATCC 1

RESULT 18

US-11-036-317-121303/c
; Sequence 121303, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 121303
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-121303

Query Match 2.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 507 AGCCGGCCAGGGCTTTATAGCCACC 531
Db 25 AGCCGGCCAGGGCTTTATAGCCACC 1

RESULT 19

US-11-036-317-122357/c
; Sequence 122357, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

; SEQ ID NO 122357
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-11-036-317-122357

Query Match 2.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 297 CTGCCCGCTGTACCCGAGTTTTCAC 321
|
Db 25 CTGCCCGCTGTACCCGAGTTTTCAC 1

RESULT 20

US-11-036-317-124848/c
; Sequence 124848, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 124848
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-11-036-317-124848

Query Match 2.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 512 GCCAGGGCTTTATAGCCACCTCTTA 536
|
Db 25 GCCAGGGCTTTATAGCCACCTCTTA 1

RESULT 21

US-11-036-317-137071/c
; Sequence 137071, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 137071
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-11-036-317-137071

Query Match 2.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 388 CCCGGGAAGGTCACCAAGAGCGGA 412
|
Db 25 CCCGGGAAGGTCACCAAGAGCGGA 1

RESULT 22

US-11-036-317-138129/c
; Sequence 138129, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 138129
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-11-036-317-138129

Query Match 2.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 445 TGGTTGAACCTTATCTGCGCATCGA 469
|
Db 25 TGGTTGAACCTTATCTGCGCATCGA 1

RESULT 23

US-11-036-317-148396/c
; Sequence 148396, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 148396
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-11-036-317-148396

Query Match 2.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 349 GTTGGGTCTTCGCTATCACAGCCA 373
|
Db 25 GTTGGGTCTTCGCTATCACAGCCA 1

RESULT 24

US-11-036-317-565796/c
; Sequence 565796, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13

;; PRIOR APPLICATION NUMBER: US 60/536,639
;; PRIOR FILING DATE: 2004-01-13
;; NUMBER OF SEQ ID NOS: 991174
;; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
;; SEQ ID NO 565796
;; LENGTH: 25
;; TYPE: DNA
;; ORGANISM: Mus musculus

US-11-036-317-565796

Query Match 2.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 437 AGCCCTACTGTTGAACCTATCTG 461

Db 25 AGCCCTACTGTTGAACCTATCTG 1

RESULT 25

US-11-036-317-632291/c
;; Sequence 632291, Application US/11036317
;; Publication No. US20050214823A1
;; GENERAL INFORMATION:
;; APPLICANT: Williams, Alan
;; APPLICANT: Blume, John
;; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
;; FILE REFERENCE: 3654.1
;; CURRENT APPLICATION NUMBER: US/11/036,317
;; CURRENT FILING DATE: 2005-01-13
;; PRIOR APPLICATION NUMBER: US 60/536,639
;; PRIOR FILING DATE: 2004-01-13
;; NUMBER OF SEQ ID NOS: 991174
;; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
;; SEQ ID NO 632291
;; LENGTH: 25
;; TYPE: DNA
;; ORGANISM: Mus musculus

US-11-036-317-632291

Query Match 2.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 335 CAGCCTTGCCACAGTTGGTCTTC 359

Db 25 CAGCCTTGCCACAGTTGGTCTTC 1

RESULT 26

US-11-036-317-699875/c
;; Sequence 699875, Application US/11036317
;; Publication No. US20050214823A1
;; GENERAL INFORMATION:
;; APPLICANT: Williams, Alan
;; APPLICANT: Blume, John
;; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
;; FILE REFERENCE: 3654.1
;; CURRENT APPLICATION NUMBER: US/11/036,317
;; CURRENT FILING DATE: 2005-01-13
;; PRIOR APPLICATION NUMBER: US 60/536,639
;; PRIOR FILING DATE: 2004-01-13
;; NUMBER OF SEQ ID NOS: 991174
;; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
;; SEQ ID NO 699875
;; LENGTH: 25
;; TYPE: DNA
;; ORGANISM: Mus musculus

US-11-036-317-699875

Query Match 2.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 460 TGGCATCGAGCAGTTCGGAATCC 484

Db 25 TGGCATCGAGCAGTTCGGAATCC 1

RESULT 27

US-11-036-317-704471/c
;; Sequence 704471, Application US/11036317
;; Publication No. US20050214823A1
;; GENERAL INFORMATION:
;; APPLICANT: Williams, Alan
;; APPLICANT: Blume, John
;; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
;; FILE REFERENCE: 3654.1
;; CURRENT APPLICATION NUMBER: US/11/036,317
;; CURRENT FILING DATE: 2005-01-13
;; PRIOR APPLICATION NUMBER: US 60/536,639
;; PRIOR FILING DATE: 2004-01-13
;; NUMBER OF SEQ ID NOS: 991174
;; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
;; SEQ ID NO 704471
;; LENGTH: 25
;; TYPE: DNA
;; ORGANISM: Mus musculus

US-11-036-317-704471

Query Match 2.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 265 GTCTTGGCCTGACCGCTCTGGATCC 289

Db 25 GTCTTGGCCTGACCGCTCTGGATCC 1

RESULT 28

US-11-036-317-720585/c
;; Sequence 720585, Application US/11036317
;; Publication No. US20050214823A1
;; GENERAL INFORMATION:
;; APPLICANT: Williams, Alan
;; APPLICANT: Blume, John
;; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
;; FILE REFERENCE: 3654.1
;; CURRENT APPLICATION NUMBER: US/11/036,317
;; CURRENT FILING DATE: 2005-01-13
;; PRIOR APPLICATION NUMBER: US 60/536,639
;; PRIOR FILING DATE: 2004-01-13
;; NUMBER OF SEQ ID NOS: 991174
;; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
;; SEQ ID NO 720585
;; LENGTH: 25
;; TYPE: DNA
;; ORGANISM: Mus musculus

US-11-036-317-720585

Query Match 2.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 507 AGCCGCCAGGCGCTTTATAGCCACC 531

Db 25 AGCCGCCAGGCGCTTTATAGCCACC 1

RESULT 29

US-11-036-317-726995/c
;; Sequence 726995, Application US/11036317
;; Publication No. US20050214823A1
;; GENERAL INFORMATION:
;; APPLICANT: Williams, Alan
;; APPLICANT: Blume, John

```
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 726995
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-726995

Query Match          2.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 297 CTGCCGCTGTACCCGAGTTTTCAC 321
      |||||
Db 25 CTGCCGCTGTACCCGAGTTTTCAC 1

RESULT 30
US-11-036-317-737834/c
; Sequence 737834, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 737834
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-737834

Query Match          2.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 512 GCCAGGGCTTTATAGCCACCTCTTA 536
      |||||
Db 25 GCCAGGGCTTTATAGCCACCTCTTA 1

RESULT 31
US-11-036-317-775667/c
; Sequence 775667, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 775667
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-775667
```

```
Query Match          2.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 388 CCGGGAAGGTCAACCAAGAGCGGA 412
      |||||
Db 25 CCGGGAAGGTCAACCAAGAGCGGA 1

RESULT 32
US-11-036-317-780021/c
; Sequence 780021, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 780021
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-780021

Query Match          2.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 445 TGGTTGAACCCCTATCTGCGCATCGA 469
      |||||
Db 25 TGGTTGAACCCCTATCTGCGCATCGA 1

RESULT 33
US-11-036-317-819409/c
; Sequence 819409, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 819409
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-819409

Query Match          2.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 349 GTTGGGTCTTCGCTATCACACGCCA 373
      |||||
Db 25 GTTGGGTCTTCGCTATCACACGCCA 1

RESULT 34
US-10-014-774-1/c
; Sequence 1, Application US/10014774
```



```

; Publication No. US20020099173A1
; GENERAL INFORMATION:
; APPLICANT: D'Azzo, Alessandra
; APPLICANT: Bongiovanni, Antonella
; APPLICANT: Nastasi, Tommaso
; TITLE OF INVENTION: Protein Specific for Cardiac and Skeletal Muscle
; FILE REFERENCE: 2427/1F509-US1
; CURRENT APPLICATION NUMBER: US/10/014,774
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: PCT/US00/11900
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/131,814
; PRIOR FILING DATE: 1999-04-29
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1036
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-014-774-1

Query Match      2.1%; Score 22; DB 1; Length 1036;
Best Local Similarity 51.0%; Pred. No. 1.2;
Matches 52; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

Qy 221 AGTGGAAATTCAGGAAAGAGCTGGCTGGTGGCGGCACCTAGCTCTTGGCCCTGACCGC 280
Db 322 AGTGGAAATTCAGGAAAGAGCTGGCTGGTGGCGGCACCTAGCTCTTGGCCCTGACCGC 280

Qy 281 TCTGGATCCCCCGCAGTCTGGCGCTGTACCCGAGTCTTCACT 322
Db 262 AGTGGCCCGCACCGCCAGCTCTTTCTCAATTTCCACT 221

RESULT 35
US-10-014-774-14
; Sequence 14, Application US/10014774
; Publication No. US20020099173A1
; GENERAL INFORMATION:
; APPLICANT: D'Azzo, Alessandra
; APPLICANT: Bongiovanni, Antonella
; APPLICANT: Nastasi, Tommaso
; TITLE OF INVENTION: Protein Specific for Cardiac and Skeletal Muscle
; FILE REFERENCE: 2427/1F509-US1
; CURRENT APPLICATION NUMBER: US/10/014,774
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: PCT/US00/11900
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/131,814
; PRIOR FILING DATE: 1999-04-29
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 499
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-014-774-14

Query Match      1.9%; Score 20; DB 1; Length 499;
Best Local Similarity 61.5%; Pred. No. 2.5;
Matches 32; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

Qy 640 TCATCAACGGGAGACATGGCCCTAGCGCCCGGGGCTGCCAGCTGCTCA 691
Db 73 TGAGCAGCTGGCAGCCCCCGCGCGCTAGGGCCCATGTCTCCCGTTGATGA 124

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Search completed: March 2, 2006, 10:56:45
Job time : 2 secs

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1015 CTGAGAAAAAATAAAAAA 1036

Matches	22:	Conservative	0:	Mismatches	0:	Indels	0:	Gaps	0:
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RESULT 2
US-10-310-914A-351295/C
; Sequence 351295, Application US/10310914A

; GENERAL INFORMATION:
 ; APPLICANT: Bentwich, Isaac
 ; APPLICANT: Shiller, Kvuzat

APPLICANT: Shiller, Kuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory g

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; TITLE OF INVENTION:  uses channel
;
; FILE REFERENCE: 06087.0200.CPUS01
;
; CURRENT APPLICATION NUMBER: US/10/310.914A
;

```

; CURRENT FILING DATE: 2002-12-06
 ; NUMBER OF SEQ ID NOS: 1388402
 ;

```

; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 351295

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;
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
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US-10-310-914A-351295

Query Match	2.0%;	Score 21;	DB 1;	Length 21;
Best Local Similarity	100.0%;	Pred. No. 1.8;		
Matches 21;	Conservative	0;	Mismatches	0;
Indels	0;	Gaps	0;	

RESULT 3

```

RESULT 3
US-10-310-914A-869839/c
; Sequence 869839, Application US/10310914A
; Publication No. US2006003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01

```

; CURRENT FILING DATE: 2002-12-06
 ; NUMBER OF SEC ID NOS: 1388402

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? CURRENT FILING DATE: 2002-12-06
?
? NUMBER OF SEQ ID NOS: 1388402
?
? SOFTWARE: PatentIn version 3.3
?
? SEQ ID NO 869839
?

```

```

; LENGTH: 21
;
; TYPE: RNA
;
; ORGANISM: Human
;
US-10-310-914A-869839

```

```

Query Match      2.0% Score 21; DB 1; Length 21;
Best local Similarity 100.0%; Pred. No. 1-8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0

```

QY	1015	CTGAGAAAAAAAAAAAAAAAAA	1035
Db	21	CTGAGAAAAAAAAAAAAAAAAA	1

RESULT 4

```

US-10-310-914A-916337/C
: Sequence 916337, Application US/10310914A
: Publication No. US2006003322A1
: GENERAL INFORMATION:
: APPLICANT: Bentwich, Isaac
: APPLICANT: Shlier, Kuzat
: TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory s

```

; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 916337
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-916337

Query Match 2.0%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.8; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1015 CTCGAGAAAAA 1035
Db 21 CTCGAGAAAAA 1

RESULT 5

US-10-310-914A-1020143/c
; Sequence 1020143, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1020143
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1020143

Query Match 2.0%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.8; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1015 CTCGAGAAAAA 1035
Db 21 CTCGAGAAAAA 1

RESULT 6

US-10-310-914A-589295/c
; Sequence 589295, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 589295
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-589295

Query Match 2.0%; Score 21; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.7; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1015 CTCGAGAAAAA 1035
Db 21 CTCGAGAAAAA 1

Search completed: March 2, 2006, 10:57:51
Job time : 0.001 secs

Query Match	100.0%;	Score 970;	DB 1;	Length 970;
Best Local Similarity	100.0%;	Pred. No. 0.0011;		

BC074737 916 bp mRNA linear PRI 04-AUG-2004
 DEFINITION Homo sapiens neuralized-like 2 (Drosophila), mRNA (cDNA clone
 MGC:103813 IMAGE:30915194), complete cds.
 ACCESSION BC074737
 VERSION BC074737.2 GI:50960526
 KEYWORDS MGC.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.
 REFERENCE 1 (bases 1 to 916)
 AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
 Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
 Altschul, S.F., Zeeberg, B., Buettow, K.H., Schaefer, C.F., Bhat, N.K.,
 Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
 Datchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
 Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
 Scheetz, T.E., Brownstein, M.J., Ustin, T.B., Toshiyuki, S.,
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 Generation and initial analysis of more than 15,000 full-length
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 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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 DIRECTOR MGC Project.
 DIRECT SUBMISSION
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 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 NTH-MGC Project URL: <http://mgc.nci.nih.gov>
 On Aug 4, 2004 this sequence version replaced gi:49902602.
 CONTACT: MGC help desk
 EMAIL: cgaps-remail.nih.gov
 TISSUE Procurement: Genome Sequence Centre, British Columbia Cancer
 Center
 cDNA Library Preparation: British Columbia Cancer Research Center
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Genome Sequence Centre,
 BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
 Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield,
 Andy Chan, Steve S. Chand, William Chow, Allison Cloutier, Ruth
 Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao,
 Kim MacDonald, Anara Masson, Mike R. Mayo, Josh Moran, Ryan Morin,
 Telka Olson, Diana Palmquist, Anca Petrescu, Anna Liisa Prahbu,
 Parvaneh Saeedi, JR Santos, Angélique Schnerch, Ursula Skalska,
 Duane Smalish, Jeff Stott, Miranda Tsai, George Yang, Jacquie
 Schein, Asim Siddiqui, Rob Holt, Marco Marra.
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VERSION Q0727380.1 GI:42293202
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Hominidae; Homo.
REFERENCE
AUTHORS Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
TITLE Kites, such as nucleic acid arrays, comprising a majority of
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thereof
JOURNAL Patent: WO 02068579-A 13314 06-SEP-2002;
PE Corporation (NY) (US)
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

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Run on: March 2, 2006, 10:21:36 ; Search time 2 Seconds
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Title: US-10-014-774-3

Perfect score: 970

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Scoring table: IDENTITY_NUC

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Searched: 5 seqs, 3629 residues

Total number of hits satisfying chosen parameters: 10

Minimum DB seq length: 0

Maximum DB seq length: 970

Post-processing: Minimum Match 0%

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Listing first 5 summaries

Database : us-10-014-774-3.sl.rst4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1 (bases 1 to 858)
Hubisz, M.J., Fladel-Alon, A., Tanenbaum, D.M., Civello, D.,
White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
A Scan for Positively Selected Genes in the Genomes of Humans and
Chimpanzees
Chimpanzees
(er) PLOS Biol. 3 (6), E170 (2005)
PUBLISHED 15869325
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AUTHORS Nielsen, R., Bustamante, C., Clark, A.G., Gnanowski, S., Sackton, T.B.,

Hubisz, M.J., Fladel-Alon, A., Tanenbaum, D.M., Civello, D.,
White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
Direct Submission
Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
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DEFINITION AL844375
ACCESSION AL844375
VERSION AL844375.1 GI:22019153
KEYWORDS EST.
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Hominae; Homo
1 (bases 1 to 581)
Ashcroft, K., Bethel, G., Bye, J. M., Howell, G. R., Huckle, E. J. and
Sheridan, E.
Homo sapiens EST sequence
Unpublished (2002)
Contact: The Sanger Centre
The Sanger Centre
Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK
Email: humquery@sanger.ac.uk
Sanger Centre name : sccdl1472.1587085
Homo sapiens EST sequence. This sequence was generated as part of
The Wellcome Trust Sanger Institute program to identify and
annotate genes in the human genome. Incomplete or unconfirmed genes
are experimentally analysed using a variety of cDNA library
resources. This sequence was obtained from a PCR product generated
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http://www.sanger.ac.uk/Teams/Team69/.

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

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Maximum Match 100%
Listing first 3 summaries

Database : us-10-014-774-3.sl.rng4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	970	100.0	970	1 AAA89044	Human muscle-speci
2	573	59.1	574	1 ACH90886	Human genome deriv
3	250	25.8	250	1 ABX75864	Human Neu4 cDNA.

ALIGNMENTS

RESULT 1
AAA89044
ID AAA89044 standard; cDNA; 970 BP.

XX AC AAA89044;
XX DT 05-MAR-2001 (first entry)
XX DE Human muscle-specific protein Ozz cDNA.

XX KW Ozz; human; muscle-specific protein; myogenesis; muscle damage;
XX KW galactosialidosis; myocardial infarction; angina; therapy; diagnosis;
XX KW Chromosome 20; ss.

XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX CDS 20..877
FT /*tag= a

XX PN WO200066733-A1.

XX PD 09-NOV-2000.

XX PF 28-APR-2000; 2000WO-US011900.

XX PR 29-APR-1999; 99US-0131814P.
XX PA (STUD-) ST JUDE CHILDREN'S RES HOSPITAL.
XX PI D'azzo A, Bongiovanni A, Nastasi T;
XX WPI; 2001-007221/01.
XX P-PSDB; AAB19851.
XX Novel protein Ozz and nucleic acid encoding the protein involved in
XX development and function of muscle, useful as target for identifying
XX drugs effective in treating myogenesis disorders.
XX PS Claim 12; Fig 2B; 62pp; English.
XX CC The present sequence is that of cDNA encoding a novel human muscle-
XX specific protein, termed Ozz (see AAB19851), that regulates development
XX and function of muscle cells. The human Ozz gene was located on
XX chromosome 20 (PPGB locus). The cDNA shows 85% homology to murine Ozz
XX cDNA (see AAA89043). The murine Ozz protein is preferentially expressed
XX by a 1.0 kb mRNA in heart and skeletal muscle. Human and mouse proteins
XX share homology with neuralised proteins, which are associated with a
XX number of muscle proteins, including beta-catenin. Ozz protein is useful
XX for detecting damage to muscle tissue or disease associated with a defect
XX in Ozz expression. Increase in the level of Ozz protein in blood or in a
XX blood fraction indicates damage to muscle tissue in the heart and an
XX abnormal level or localization of Ozz in muscle cells from the atrium of
XX the heart of a subject is useful for detecting galactosialidosis
XX (claimed). The presence of Ozz in blood or a blood fraction indicates
XX muscle tissue damage e.g. ischaemia associated with either unstable
XX angina, myocardial infarction or both. Nucleotide sequences derived from
XX the gene encoding Ozz and peptide sequences derived from Ozz are useful
XX as targets to identify drugs that are effective in treating myogenesis
XX disorders
XX SQ Sequence 970 BP; 157 A; 345 C; 296 G; 172 T; 0 U; 0 Other;

Query Match	100.0%;	Score 970;	DB 1;	Length 970;
Best Local Similarity	100.0%;	Pred. No. 0.00048;		
Matches 970;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Oy 1	CCTGCCCTATGGCCGAGAGATGGCTGCTGCTCCGAGCCCGTGGATTCCGGTGCACCTCTG	60		
Db 1	CCTGCCCTATGGCCGAGAGATGGCTGCTGCTCCGAGCCCGTGGATTCCGGTGCACCTCTG	60		
Oy 61	GGGACTGAGCGCCCGGAGCCCTCCACCCGCTTCATCGGTGACGGTGCCCAACAT	120		
Db 61	GGGACTGAGCGCCCGGAGCCCTCCACCCGCTTCATCGGTGACGGTGCCCAACAT	120		
Oy 121	CCGGTGGACCCCTCTGGGACGCGGGCCACACGGCTGGAGAGCTTCGCCCCACGGGTGTG	180		
Db 121	CCGGTGGACCCCTCTGGGACGCGGGCCACACGGCTGGAGAGCTTCGCCCCACGGGTGTG	180		
Oy 181	CTTCAGCCGCGAGCGCTGGCCCGGGCCAGGTCTTCTGTCGAGATCGAGGAGAAAGA	240		
Db 181	CTTCAGCCGCGAGCGCTGGCCCGGGCCAGGTCTTCTGTCGAGATCGAGGAGAAAGA	240		
Oy 241	GCTGGGCTGGTGGGACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	300		
Db 241	GCTGGGCTGGTGGGACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	300		
Oy 301	CCCCGTTCCCGAGTTTCTCTGCGCCGATCTGCTGCGGATCTGCTGCGGCCACACCTTGGG	360		
Db 301	CCCCGTTCCCGAGTTTCTCTGCGCCGATCTGCTGCGGATCTGCTGCGGCCACACCTTGGG	360		
Oy 361	CATCAGCGCCACCAACACCGCGTCCCGGGAGGGCCCGCGAGGCGGAGGCGGCGGC	420		
Db 361	CATCAGCGCCACCAACACCGCGTCCCGGGAGGGCCCGCGAGGCGGAGGCGGCGGC	420		
Oy 421	CCCCAGCGGACCTCCAAACCTCTCTGTTGAACCATATCTGCGCATTTGAGCATTTTCGCAT	480		
Db 421	CCCCAGCGGACCTCCAAACCTCTCTGTTGAACCATATCTGCGCATTTGAGCATTTTCGCAT	480		

Qy	481	TCCCGGGACCGCCTCGTGGGCGCAGCCGCGCAGGGCTCTACAGCCATCTCTTGGACCA	540
Db	481	TCCCGGGACCGCCTCGTGGGCGCAGCCGCGCAGGGCTCTACAGCCATCTCTTGGACCA	540
Qy	541	GCTCTATGAGCTGAACGTGCTGCCTCCGACCGCGCGCGGTAGCGCCTGGGTGCTCTCTT	600
Db	541	GCTCTATGAGCTGAACGTGCTGCCTCCGACCGCGCGCGGTAGCGCCTGGGTGCTCTCTT	600
Qy	601	TTGCCGCGCCCGGATGGCAGCGCGCAGATCACAATCATCAACGCGCAGGACATGGG	660
Db	601	TTGCCGCGCCCGGATGGCAGCGCGCAGATCACAATCATCAACGCGCAGGACATGGG	660
Qy	661	CCGAGCGCCCGGGGACTGCCAGCTGCGCAGCCCTCTACGCGTGGTGGACGTGTTGC	720
Db	661	CCGAGCGCCCGGGGACTGCCAGCTGCGCAGCCCTCTACGCGTGGTGGACGTGTTGC	720
Qy	721	TTCCACAAAGAGCGTGGCGCTTTCCAGCTCGAGTATGGCTTGGCATCCCTGCAGACTCT	780
Db	721	TTCCACAAAGAGCGTGGCGCTTTCCAGCTCGAGTATGGCTTGGCATCCCTGCAGACTCT	780
Qy	781	GTGCGCCTAGTGATACAAAGAGCAGTGGTGCACCGGCTGGCCATTGATGGGCTCCACCT	840
Db	781	GTGCGCCTAGTGATACAAAGAGCAGTGGTGCACCGGCTGGCCATTGATGGGCTCCACCT	840
Qy	841	GCCCAAGAACTTAAAGGATTTCTGCAAGTATGAGTGAAGACCCACAGTGCACGAGCAC	900
Db	841	GCCCAAGAACTTAAAGGATTTCTGCAAGTATGAGTGAAGACCCACAGTGCACGAGCAC	900
Qy	901	AGTGTGATCCTGGAGCCCGACACTGTGGCTGGTTCGAGTTGGCCACCATTTGCTGTCG	960
Db	901	AGTGTGATCCTGGAGCCCGACACTGTGGCTGGTTCGAGTTGGCCACCATTTGCTGTCG	960
Qy	961	CAGCCAAGAC	970
Db	961	CAGCCAAGAC	970
RESULT 2			
ACH90886			
ID ACH90886 standard; DNA; 574 BP.			
XX	ACH90886;		
XX	29-JUL-2004 (first entry)		
DT	Human genome derived single exon probe #24081.		
DE	Human; probe; ss; gene expression; single exon probe; microarray;		
KW	alternative splicing event; genomic alteration.		
KW	Homo sapiens.		
OS	US2003194704-A1.		
XX	16-OCT-2003.		
XX	03-APR-2002; 2002US-00029386.		
PF	03-APR-2002; 2002US-00029386.		
XX	(PENN/) PENN S G.		
XX	(RANK/) RANK D R.		
PA	(HANZ/) HANZEL D K.		
XX	Penn SG, Rank DR, Hanzel DK;		
XX	WPI; 2004-119264/12.		
XX	New human genome-derived single exon nucleic acid probes useful for human		
PT	gene expression analysis, for identifying or characterizing alternative		
PT	splicing events, for assessing genomic alterations or as tools for		
PT	surveying tissues.		

Qy 609 GCCCGGATGACGGCCGACATGACATCATCAACGCGAGGACATGGCCCGGAGCG 668
Db 421 GCCCGGATGACGGCCGACATGACATCATCAACGCGAGGACATGGCCCGGAGCG 480
Qy 669 CCCGGGAGCTGCCAGCTGCGCAGCCCTCTACGCGGTGGTGGACGTGTGCTTCCCAA 728
Db 481 CCCGGGAGCTGCCAGCTGCGCAGCCCTCTACGCGGTGGTGGACGTGTGCTTCCCAA 540
Qy 729 AGACGCTGCGCTGTTCAGCTCGAGTATGGCT 761
Db 541 AGACGCTGCGCTGTTCAGCTCGAGTATGGCT 573

RESULT 3

ID ABX75864 standard; cDNA; 250 BP.

XX AC

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Query Match

Best Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

Other

Score

DB

Length

250

100.0%

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Qy 92 CGCTTCCATCGGGTGCACGGTGCACCAACATCGCGGTGACCCCTCTGGAGCGGGCCACA 151

Db 1 CGCTTCCATCGGGTGCACGGTGCACCAACATCGCGGTGACCCCTCTGGAGCGGGCCACA 60

Qy 152 CGCGTGGAGAGCTTCGCCACCGGCTGTCTTACAGCCGCGAGCCGCTGGCCCGGGCCAG 211

Db 61 CGCGTGGAGAGCTTCGCCACCGGCTGTCTTACAGCCGCGAGCCGCTGGCCCGGGCCAG 120

Qy 212 GTCTTCTCTGCTCGAGATCGAGGAGAAAGAGCTGGGCTGGTGGGACATCTCGCTCTCGGT 271

Db 121 GTCTTCTCTGCTCGAGATCGAGGAGAAAGAGCTGGGCTGGTGGGACATCTCGCTCTCGGT 180

Qy 272 CTGACCGCGCTGGACCCCGCCAGTCTGGCCCGCCCGTTCCTCCGAGTTTCTCTGCCCGATCTG 331

Db 181 CTGACCGCGCTGGACCCCGCCAGTCTGGCCCGCCCGTTCCTCCGAGTTTCTCTGCCCGATCTG 240

Qy 332 GTCAACCTGG 341

Db 241 GTCAACCTGG 250

Search completed: March 2, 2006, 10:22:55

Job time : 2 secs

Novel neuralized polypeptide, Neu useful for controlling cell proliferation and calcium signaling induced transcriptional processes and treating depression, pain, anxiety, cancer and neurodegenerative diseases.

Claim 6: Page 49; 75pp; English.

The invention relates to a purified neuralised (Neu) polypeptide comprising at least one neuralised homology repeat (NHR) domain and a C3HC4 RING-zinc finger domain, and a polynucleotide encoding the polypeptide. The polynucleotide is useful for constructing a transformed host cell that expresses a Neu protein. Neu has neurogenic function and functions as a transcriptional regulator, as a calcium-signal transducer, in cell signalling and synaptogenesis, in memory learning, tumorigenesis, myogenesis and development of other organ systems and is related to repair and regeneration after injury to the central nervous system. Neu interacts with neurogenic genes, proteins implicated in nuclear transport and with Parkin-like proteins. Neu has the potential to interfere with inductive tissue interactions, cytokine signalling, RNA processing, early immediate responses, death of specific cell populations, nuclear hormone receptor signalling and axonal path-finding. The Neu family of proteins presents a set of diagnostic and therapeutic

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 2, 2006, 10:27:41 ; Search time 1 Seconds
(without alignments)
3.480 Million cell updates/sec

Title: US-10-014-774-3
Perfect score: 970
Sequence: 1 ccgcgcctatgcccagagaga.....acattgctccagccagagac 970

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 0.5

Searched: 3 segs, 1794 residues

Total number of hits satisfying chosen parameters: 6

Minimum DB seq length: 0
Maximum DB seq length: 970

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 3 summaries

Database: us-10-014-774-3.sl.rnpbms.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	970	100.0	970	1	US-10-014-774-3
2	573	59.1	574	1	US-10-029-386-24081
3	250	25.8	250	1	US-09-808-387-33

ALIGNMENTS

RESULT 1
US-10-014-774-3

Sequence 3, Application US/10014774
Publication No. US20020099173A1

GENERAL INFORMATION:

APPLICANT: D'Azzo, Alessandra

APPLICANT: Bongiovanni, Antonella

APPLICANT: Nascetti, Tommaso

TITLE OF INVENTION: Protein Specific for Cardiac and Skeletal Muscle

FILE REFERENCE: 2427/1P509-US1

CURRENT APPLICATION NUMBER: US/10/014,774

PRIOR FILING DATE: 2001-10-29

PRIOR APPLICATION NUMBER: PCT/US00/11900

PRIOR FILING DATE: 2000-04-28

PRIOR APPLICATION NUMBER: US 60/131,814

NUMBER OF SEQ ID NOS: 24

SOFTWARE: PseSeq for Windows Version 3.0

SEQ ID NO 3

LENGTH: 970

TYPE: DNA

ORGANISM: Homo sapiens

US-10-014-774-3

Query Match 100.0%; Score 970; DB 1; Length 970;

Best Local Similarity 100.0%; Pred. No. 0.00048;
Matches 970; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	CTTGCCCTATGCGGAGAGATGCTGCTCTCCGAGCCCTGGATTCGGGTGACACTG 60
DB	1	CTTGCCCTATGCGGAGAGATGCTGCTCTCCGAGCCCTGGATTCGGGTGACACTG 60
QY	61	GGGACTGAGGCGCCGAGGCGCCCTCCACCCGCTTCATCGGGTGCAGGTGCACAT 120
DB	61	GGGACTGAGGCGCCGAGGCGCCCTCCACCCGCTTCATCGGGTGCAGGTGCACAT 120
QY	121	CCGCTGAGACCCCTCTGAGAGCGAGGCGCACAGCGGTGAGAGCTTCCGACAGCGGTG 180
DB	121	CCGCTGAGACCCCTCTGAGAGCGAGGCGCACAGCGGTGAGAGCTTCCGACAGCGGTG 180
QY	181	CTTGAGCCGAGAGCGCTGCGCCCGGAGAGCTTCTGCTGAGATCGAGAGAGAAAGA 240
DB	181	CTTGAGCCGAGAGCGCTGCGCCCGGAGAGCTTCTGCTGAGATCGAGAGAGAAAGA 240
QY	241	GCTGGCTGAGGCGGAGCATGAGGCTGAGCTGAGCGGCTGAGACCCGCAAGTCTGAC 300
DB	241	GCTGGCTGAGGCGGAGCATGAGGCTGAGCTGAGCGGCTGAGACCCGCAAGTCTGAC 300
QY	301	CCCGCTCCGAGTTTCTCTGCGGATCTGATCAACTGAGGCGCACACTGAGTCTTGC 360
DB	301	CCCGCTCCGAGTTTCTCTGCGGATCTGATCAACTGAGGCGCACACTGAGTCTTGC 360
QY	361	CATCAAGGCGCACCAACAGCGGTGCGCCGAGAGGCGCCGCGGAGGCGGAGGCGGCG 420
DB	361	CATCAAGGCGCACCAACAGCGGTGCGCCGAGAGGCGCCGCGGAGGCGGAGGCGGCG 420
QY	421	CCCGAGCGGAGCTCCAACTCTCTGAGAGCAATATCGGAGCATGAGAGGTTGCGAT 480
DB	421	CCCGAGCGGAGCTCCAACTCTCTGAGAGCAATATCGGAGCATGAGAGGTTGCGAT 480
QY	481	TCCCGGAGAGCGGCTGAGGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 540
DB	481	TCCCGGAGAGCGGCTGAGGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 540
QY	541	GCTCTATAGAGTGAACGTGCTGCTCCGAGCGGCGGAGGAGCGGCTGAGTCTCTT 600
DB	541	GCTCTATAGAGTGAACGTGCTGCTCCGAGCGGCGGAGGAGCGGCTGAGTCTCTT 600
QY	601	TGCGCGGCGGCGGAGTGCACGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGG 660
DB	601	TGCGCGGCGGCGGAGTGCACGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGG 660
QY	661	CCCGAGCGGCGGAGTGCACGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGG 720
DB	661	CCCGAGCGGCGGAGTGCACGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGG 720
QY	721	TTTCAAAAGAGCGTGCCTTGTCAAGTGCAGTGCAGTGCAGTGCAGTGCAGTGC 780
DB	721	TTTCAAAAGAGCGTGCCTTGTCAAGTGCAGTGCAGTGCAGTGCAGTGCAGTGC 780
QY	781	GTGCGGCTGAGTGAACAAAGAGAGTGCAGCGGCTGAGCTGAGTGCAGTGCAGT 840
DB	781	GTGCGGCTGAGTGAACAAAGAGAGTGCAGCGGCTGAGCTGAGTGCAGTGCAGT 840
QY	841	GGCGAAAGAACTTAAGATTTCTGCAAGTATGAGTGAAGACCAAGTGCAGCAAG 900
DB	841	GGCGAAAGAACTTAAGATTTCTGCAAGTATGAGTGAAGACCAAGTGCAGCAAG 900
QY	901	AGCTGATCTGAGAGCCCAAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
DB	901	AGCTGATCTGAGAGCCCAAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
QY	961	CAGCCAGAGC 970
DB	961	CAGCCAGAGC 970

RESULT 2

```

US-10-029-386-24081
Sequence 24081, Application US/10029386
Publication NO. US20030194704A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR C
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: AEOICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 24081
LENGTH: 574
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AL008726.1
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.3
OTHER INFORMATION: SWISSPROT HIT: P29503, EVALUE 1.30e-01
OTHER INFORMATION: NT HIT: G16679436, EVALUE 5.00e-29
OTHER INFORMATION: EST_HUMAN HIT: AW515245.1, EVALUE 0.00e+00
US-10-029-386-24081

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Query Match	59.1%;	Score 573;	DB 1;	Length 574;
Best Local Similarity	100.0%;	Pred. No. 0.049;		
Matches 573;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

Oy	189	GCAGAGCCGTGAGCCCGGGAGCAGGCTTCTCGATGATCGAGGAGAAAGCTGGGCT	248
Db	1	GCAGAGCCGTGAGCCCGGGAGCAGGCTTCTCGATGATCGAGGAGAAAGCTGGGCT	60
Oy	249	GATGCGGACATCTGCGTCTCGATCTGACCGCGCTGAGACCCCGCAGTCTGAGCCCGCTTC	308
Db	61	GATGCGGACATCTGCGTCTCGATCTGACCGCGCTGAGACCCCGCAGTCTGAGCCCGCTTC	120
Oy	309	CCGAGTTTCTCTGCGCGATCTGATCAACTGAGGCAACACTGGGCTCTTCGTCATCAAGC	368
Db	121	CCGAGTTTCTCTGCGCGATCTGATCAACTGAGGCAACACTGGGCTCTTCGTCATCAAGC	180
Oy	369	GCGACCAACAACGGGTGCCCCGGGAGGGGCGCCCGGAGCGGAGCAGCGGCCCCAGCC	428
Db	181	GCGACCAACAACGGGTGCCCCGGGAGGGGCGCCCGGAGCGGAGCAGCGGCCCCAGCC	240
Oy	429	GACCTCCAACTCTCTCGTGAACCATATCTGCGATTGAGCAGTTTCGCTATCCCGGG	488
Db	241	GACCTCCAACTCTCTCGTGAACCATATCTGCGATTGAGCAGTTTCGCTATCCCGGG	300
Oy	489	ACCGCTTGATGGGCGGACGCGGGCGAGGGCTCTAACGCCATCTTGGACAACAGCTTATG	548
Db	301	ACCGCTTGATGGGCGGACGCGGGCGAGGGCTCTAACGCCATCTTGGACAACAGCTTATG	360
Oy	549	AGCTGAAGTGTGTGCTCCGACCGGGGCGCGTGAAGCGCTGGGATCTCTTTGGCCGCG	608
Db	361	AGCTGAAGTGTGTGCTCCGACCGGGGCGCGTGAAGCGCTGGGATCTCTTTTGGCCGCG	420
Oy	609	GCCCCGATGACAGGCGCCGACATGACATCATCAACAAGCGAGGACATGAGCGCCGAGCG	668
Db	421	GCCCCGATGACAGGCGCCGACATGACATCATCAACAAGCGAGGACATGAGCGCCGAGCG	480
Oy	669	CCCGGGGACTGCACTGCGGACGCGGAGCCCTCTCAAGCGGTGGTGAAGTGTTCACAA	728
Db	481	CCCGGGGACTGCACTGCGGAGCCCTCTCAAGCGGTGGTGAAGTGTTCACAA	540
Oy	729	AGAGCGTGCCTTGTCCAGCTCGAGTATAGCT	761
Db	541	AGAGCGTGCCTTGTCCAGCTCGAGTATAGCT	573

```

: Sequence 33, Application US/09808387
: Patent No. US20020132293A1
: GENERAL INFORMATION
: APPLICANT: Kaia Palm
: APPLICANT: Tonis Timmek
: APPLICANT: Cemines Research
: TITLE OF INVENTION: MAMMALIAN NEURALIZED FAMILY OF
: TITLE OF INVENTION: TRANSCRIPTION REGULATORS AND USES THEREFOR
: FILE REFERENCE: CEMMES_001A
: CURRENT APPLICATION NUMBER: US/09/808,387
: CURRENT FILING DATE: 2001-03-14
: NUMBER OF SEQ ID NOS: 48
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 33
: LENGTH: 250
: TYPE: DNA
: ORGANISM: Homo sapien
: US-09-808-387-33

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Query Match	25.8%;	Score 250;	DB 1;	Length 250;
Best Local Similarity	100.0%;	Pred. No. 2.8;		
Matches 250;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

[illegible]

Search completed: March 2, 2006, 10:27:43
Job time : 1 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.
OM nucleic - nucleic search, using sw model
Run on: March 2, 2006, 10:29:19 ; Search time 0.001 Seconds
(without alignments)
787.640 Million cell updates/sec

Title: US-10-014-774-3
Perfect score: 970
Sequence: 1 cctgcctatggcgcagaga.....acattgctgcagccaagac 970

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 0.5

Searched: 17 seqs, 406 residues

Total number of hits satisfying chosen parameters: 34
Minimum DB seq length: 0
Maximum DB seq length: 970

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 17 summaries

Database : us-10-014-774-3.sl.rnpbn4:*
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES									
Result No.	Score	Query Match	Length	ID	Description	Score	Query Match	Length	ID
1	25	2.6	25	1	US-11-121-849-260796	25	2.6	25	1
2	25	2.6	25	1	US-11-121-849-260797	25	2.6	25	1
3	25	2.6	25	1	US-11-121-849-260798	25	2.6	25	1
4	25	2.6	25	1	US-11-121-849-260799	25	2.6	25	1
5	25	2.6	25	1	US-11-121-849-260800	25	2.6	25	1
6	25	2.6	25	1	US-11-121-849-260801	25	2.6	25	1
7	25	2.6	25	1	US-11-121-849-260802	25	2.6	25	1
8	25	2.6	25	1	US-11-121-849-260803	25	2.6	25	1
9	25	2.6	25	1	US-11-121-849-260804	25	2.6	25	1
10	25	2.6	25	1	US-11-121-849-260805	25	2.6	25	1
11	25	2.6	25	1	US-11-121-849-260806	25	2.6	25	1
12	23	2.4	23	1	US-10-310-914A-470229	23	2.4	23	1
13	23	2.4	23	1	US-10-310-914A-470237	23	2.4	23	1
14	22	2.3	22	1	US-10-310-914A-470239	22	2.3	22	1
15	21	2.2	21	1	US-10-310-914A-470228	21	2.2	21	1
16	21	2.2	21	1	US-10-310-914A-470236	21	2.2	21	1
17	21	2.2	21	1	US-10-310-914A-470238	21	2.2	21	1

ALIGNMENTS
RESULT 1
US-11-121-849-260796
; Sequence 260796, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; PRIOR FILING DATE: 2005-05-03

PRIOR APPLICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 260796
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-11-121-849-260796

Query Match 2.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.1; Indels 0;
Matches 25; Conservative 0; Mismatches 0; Gaps 0;
Qy 630 TGCACATCATCATCAACGGCGGAGGA 654
Db 1 TGCACATCATCATCAACGGCGGAGGA 25

RESULT 2
US-11-121-849-260797
; Sequence 260797, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 260797
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-260797

Query Match 2.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.1; Indels 0;
Matches 25; Conservative 0; Mismatches 0; Gaps 0;
Qy 641 ATCAACGGCGGAGGACATGGGCCCGA 665
Db 1 ATCAACGGCGGAGGACATGGGCCCGA 25

RESULT 3
US-11-121-849-260798
; Sequence 260798, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 260798
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-260798

Query Match 2.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.1; Indels 0;
Matches 25; Conservative 0; Mismatches 0; Gaps 0;

QY 693 CCCTCTACGCGTGGTGGACGTGT 717
Db 1 CCCTCTACGCGTGGTGGACGTGT 25

RESULT 4

US-11-121-849-260799
; Sequence 260799, Application US/11121849
; Publication No. US20050272080A1

GENERAL INFORMATION:

; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121.849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 260799
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien

US-11-121-849-260799

Query Match 2.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 717 TTGCTTCCACAAGAGCGTGGCGCT 741
Db 1 TTGCTTCCACAAGAGCGTGGCGCT 25

RESULT 5

US-11-121-849-260800
; Sequence 260800, Application US/11121849
; Publication No. US20050272080A1

GENERAL INFORMATION:

; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121.849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 260800
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien

US-11-121-849-260800

Query Match 2.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 735 TGGCCCTTGCTCCAGCTCGAGTATGG 759
Db 1 TGGCCCTTGCTCCAGCTCGAGTATGG 25

RESULT 6

US-11-121-849-260801
; Sequence 260801, Application US/11121849
; Publication No. US20050272080A1

GENERAL INFORMATION:

; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S

; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121.849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 260801
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien

US-11-121-849-260801

Query Match 2.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 545 TATGAGCTGAACGTGCTGCTCCGA 569
Db 1 TATGAGCTGAACGTGCTGCTCCGA 25

RESULT 7

US-11-121-849-260802
; Sequence 260802, Application US/11121849
; Publication No. US20050272080A1

GENERAL INFORMATION:

; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121.849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 260802
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien

US-11-121-849-260802

Query Match 2.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 771 TGCAGACTCTGCGCGCTAGTGAT 795
Db 1 TGCAGACTCTGCGCGCTAGTGAT 25

RESULT 8

US-11-121-849-260803
; Sequence 260803, Application US/11121849
; Publication No. US20050272080A1

GENERAL INFORMATION:

; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121.849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 260803
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien

US-11-121-849-260803

```
Query Match      2.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 777 CTCGTGCGCGCTAGTGATACAAAG 801
Db 1 CTCGTGCGCGCTAGTGATACAAAG 25

RESULT 9
US-11-121-849-260804
; Sequence 260804, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 60/567,949
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 260804
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-260804

Query Match      2.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 794 ATACAAAGGAGCATGGTGCCACCGGC 818
Db 1 ATACAAAGGAGCATGGTGCCACCGGC 25

RESULT 10
US-11-121-849-260805
; Sequence 260805, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 60/567,949
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 260805
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-260805

Query Match      2.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 576 GCCGTAGCGCGCTGGTGTCCTT 600
Db 1 GCCGTAGCGCGCTGGTGTCCTT 25

RESULT 11
US-11-121-849-260806
; Sequence 260806, Application US/11121849
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; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 60/567,949
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 260806
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-260806

Query Match      2.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 615 ATGCGACGGCGCATGCGCATCATCAT 639
Db 1 ATGCGACGGCGCATGCGCATCATCAT 25

RESULT 12
US-10-310-914A-470229/C
; Sequence 470229, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kvuzaat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 470229
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-470229

Query Match      2.4%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 6.2;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 890 CACCAGAGCACAGCTGCTCTG 912
Db 23 CACCAGAGCACAGCTGCTCTG 1

RESULT 13
US-10-310-914A-470237/C
; Sequence 470237, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kvuzaat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 470237
; LENGTH: 23
; TYPE: RNA
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; ORGANISM: Human
US-10-310-914A-470237

Query Match 2.4%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 6.2;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 941 GAAGTTGGCCACATGCTGCCAG 963
|||||
Db 23 GAAGTTGGCCACATGCTGCCAG 1

RESULT 14

US-10-310-914A-470239/c
; Sequence 470239, Application US/10310914A
; Publication No. US20060003322A1

; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac

; APPLICANT: Shiler, Kvuzat

; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and

; FILE REFERENCE: 06087.0200.CPUS01

; CURRENT APPLICATION NUMBER: US/10/310,914A

; CURRENT FILING DATE: 2002-12-06

; NUMBER OF SEQ ID NOS: 1388402

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 470239

; LENGTH: 22

; TYPE: RNA

; ORGANISM: Human

US-10-310-914A-470239

Query Match 2.3%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 7.6;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 947 GGCCACATGCTGCCAGCCAG 968
|||||
Db 22 GGCCACATGCTGCCAGCCAG 1

RESULT 15

US-10-310-914A-470228/c

; Sequence 470228, Application US/10310914A

; Publication No. US20060003322A1

; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac

; APPLICANT: Shiler, Kvuzat

; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and

; FILE REFERENCE: 06087.0200.CPUS01

; CURRENT APPLICATION NUMBER: US/10/310,914A

; CURRENT FILING DATE: 2002-12-06

; NUMBER OF SEQ ID NOS: 1388402

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 470228

; LENGTH: 21

; TYPE: RNA

; ORGANISM: Human

US-10-310-914A-470228

Query Match 2.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 892 CCAGACACAGCTGCATCTTG 912
|||||
Db 21 CCAGACACAGCTGCATCTTG 1

RESULT 16

US-10-310-914A-470236/c

; Sequence 470236, Application US/10310914A

; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 470236
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-470236

Query Match 2.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 943 AGTTGGCCACATGCTGCCAG 963
|||||
Db 21 AGTTGGCCACATGCTGCCAG 1

RESULT 17

US-10-310-914A-470238/c

; Sequence 470238, Application US/10310914A

; Publication No. US20060003322A1

; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac

; APPLICANT: Shiler, Kvuzat

; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and

; FILE REFERENCE: 06087.0200.CPUS01

; CURRENT APPLICATION NUMBER: US/10/310,914A

; CURRENT FILING DATE: 2002-12-06

; NUMBER OF SEQ ID NOS: 1388402

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 470238

; LENGTH: 21

; TYPE: RNA

; ORGANISM: Human

US-10-310-914A-470238

Query Match 2.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 882 CCACAGTGCACACAGACAG 902
|||||
Db 21 CCACAGTGCACACAGACAG 1

Search completed: March 2, 2006, 10:29:20
Job time : 1 secs